

## SEQUENCE LISTING

<110> Genentech, Inc.  
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<120> Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same

<130> 10466-14

<140> 09/665,350

<141> 2000-09-18

<150> PCT/US00/04414

<151> 2000-02-22

<150> US 60/143,048

<151> 1999-07-07

<150> US 60/145,698

<151> 1999-07-26

<150> US 60/146,222

<151> 1999-07-28

<150> PCT/US99/20594

<151> 1999-09-08

<150> PCT/US99/20944

<151> 1999-09-13

10466-14



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<212> PRT
<213> Homo sapiens
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<213> HOME 111

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20 25 30  
Arg Cys Arg Gly Leu Val Asp Lys Phe Asn Gln Gly Met Val Asp Thr  
35 40 45  
Ala Lys Lys Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Lys Thr  
50 55 60  
Leu Ser Lys Tyr Glu Ser Ser Glu Ile Arg Leu Leu Glu Ile Leu Glu  
65 70 75 80  
Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys Asn Gln Met Leu Glu Ala  
85 90 95  
Gln Glu Glu His Leu Glu Ala Trp Trp Leu Gln Leu Lys Ser Glu Tyr  
100 105 110  
Pro Asp Leu Phe Glu Trp Phe Cys Val Lys Thr Leu Lys Val Cys Cys  
115 120 125  
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130 135 140



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<211> 2206
<212> DNA
<213> Homo sapiens
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aacagccctg	gctgagggag	ctgcagcgca	gcagagtatc	tgacggcgcc	gcccggagga 240
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<213> Homo sapiens
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20 25 30  
Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu  
35 40 45  
Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala  
50 55 60  
Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile



65 70 75 80

Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln  
85 90 95

Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly  
100 105 110

Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro  
115 120 125

His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln  
130 135 140

Asp Gly Val Ala Ala Phe Glu Val Asp Val Ile Val Met Asn Ser Glu  
145 150 155 160

Gly Asn Thr Ile Leu Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr  
165 170 175

Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys  
180 185 190

Asn Glu Arg Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His  
195 200 205

Cys Glu Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys  
210 215 220

Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn  
225 230 235 240

Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys  
245 250 255

Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln  
260 265 270

Cys Glu Ile Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys  
275 280 285

Ile Gly Lys Ser Lys Cys Lys Cys Ser Lys Gly Tyr Gln Gly Asp Leu  
290 295 300

Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys  
305 310 315 320

His Glu Pro Asn Lys Cys Gln Cys Gln Glu Gly Trp His Gly Arg His  
325 330 335

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340 345 350



Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp  
370 375

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<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
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45

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oligonucleotide probe

21

<220>  
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oligonucleotide probe

22

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49



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22

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        oligonucleotide probe
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23

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<210> 11
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<213> Homo sapiens
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[illegible]



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<211> 164
<212> PRT
<213> Homo sapiens
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20 25 30  
Pro Gly Leu His Leu Arg Gly Ile Arg Asp Ala Gly Gly Arg Tyr Cys  
35 40 45  
Gln Glu Gln Asp Leu Cys Cys Arg Gly Arg Ala Asp Asp Cys Ala Leu  
50 55 60  
Pro Tyr Leu Gly Ala Ile Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr  
65 70 75 80  
Val Ser Asp Cys Cys Pro Asp Phe Trp Asp Phe Cys Leu Gly Val Pro  
85 90 95  
Pro Pro Phe Pro Pro Ile Gln Gly Cys Met His Gly Gly Arg Ile Tyr  
100 105 110  
Pro Val Leu Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln  
115 120 125  
Glu Asn Arg Gln Trp His Gly Gly Ser Arg His Asp Gln Ser His Gln  
130 135 140  
Pro Gly Gln Leu Trp Leu Ala Gly Trp Glu Pro Gln Arg Leu Leu Gly  
145 150 155 160  
His Asp Pro Gly



<210> 13  
 <211> 533  
 <212> DNA  
 <213> Homo sapiens

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 <222> (33)  
 <223> a, t, c or g

<220>  
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 <223> a, t, c or g

<220>  
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 <222> (94)  
 <223> a, t, c or g

<220>  
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 <222> (144)  
 <223> a, t, c or g

<220>  
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 <222> (188)  
 <223> a, t, c or g

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<210> 14  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 14

BB-01-000000



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<210> 15
<211> 22
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 15  
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<210> 16
<211> 50
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 16  
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<210> 17
<211> 960
<212> DNA
<213> Homo sapiens
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[illegible]

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<213> Homo sapiens
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<210> 19
<211> 24
<212> DNA
<213> Artificial Sequence
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<223> oligonucleotide probe
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<400> 19  
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<210>	20
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 20 25 30  
 Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln Leu Tyr Ser  
 35 40 45  
 Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg Arg Ile Ser Ala  
 50 55 60  
 Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu Ile Val Glu Thr Asp  
 65 70 75 80  
 Thr Phe Gly Ser Arg Val Arg Ile Lys Gly Ala Glu Ser Glu Lys Tyr  
 85 90 95  
 Ile Cys Met Asn Lys Arg Gly Lys Leu Ile Gly Lys Pro Ser Gly Lys  
 100 105 110  
 Ser Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr  
 115 120 125  
 Ala Phe Gln Asn Ala Arg His Glu Gly Trp Phe Met Ala Phe Thr Arg  
 130 135 140  
 Gln Gly Arg Pro Arg Gln Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu  
 145 150 155 160  
 Ala His Phe Ile Lys Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn  
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 195 200 205

<210> 24  
 <211> 28  
 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 24  
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<210> 25



<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 25  
 ccggtgacct gcacgtgctt gccca

24

<210> 26  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<220>  
 <221> modified\_base  
 <222> (21)  
 <223> a, t, c or g

<400> 26  
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41

<210> 27  
 <211> 2479  
 <212> DNA  
 <213> Homo sapiens

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<210> 28  
<211> 660  
<212> PRT  
<213> Homo sapiens

<400> 28  
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20 25 30  
Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn Phe Val Tyr  
35 40 45  
Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly  
50 55 60  
Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile Asn Asn Ala Gly Phe  
65 70 75 80  
Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr  
85 90 95  
Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg  
100 105 110  
Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala  
115 120 125

TGGTGTGCTGTTT



Leu Ala Gln Leu Leu Lys Leu Glu Glu Leu His Leu Asp Asp Asn Ser  
130 135 140

Ile Ser Thr Val Gly Val Glu Asp Gly Ala Phe Arg Glu Ala Ile Ser  
145 150 155 160

Leu Lys Leu Leu Phe Leu Ser Lys Asn His Leu Ser Ser Val Pro Val  
165 170 175

Gly Leu Pro Val Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile  
180 185 190

Ala Val Ile Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg  
195 200 205

Leu Ile Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly  
210 215 220

Thr Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn  
225 230 235 240

Ser Leu Ser His Pro Pro Pro Asp Leu Pro Gly Thr His Leu Ile Arg  
245 250 255

Leu Tyr Leu Gln Asp Asn Gln Ile Asn His Ile Pro Leu Thr Ala Phe  
260 265 270

Ser Asn Leu Arg Lys Leu Glu Arg Leu Asp Ile Ser Asn Asn Gln Leu  
275 280 285

Arg Met Leu Thr Gln Gly Val Phe Asp Asn Leu Ser Asn Leu Lys Gln  
290 295 300

Leu Thr Ala Arg Asn Asn Pro Trp Phe Cys Asp Cys Ser Ile Lys Trp  
305 310 315 320

Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser Ser Leu Asn Val Arg Gly  
325 330 335

Phe Met Cys Gln Gly Pro Glu Gln Val Arg Gly Met Ala Val Arg Glu  
340 345 350

Leu Asn Met Asn Leu Leu Ser Cys Pro Thr Thr Thr Pro Gly Leu Pro  
355 360 365

Leu Phe Thr Pro Ala Pro Ser Thr Ala Ser Pro Thr Thr Gln Pro Pro  
370 375 380

Thr Leu Ser Ile Pro Asn Pro Ser Arg Ser Tyr Thr Pro Pro Thr Pro  
385 390 395 400

Thr Thr Ser Lys Leu Pro Thr Ile Pro Asp Trp Asp Gly Arg Glu Arg



<210> 29  
<211> 21  
<212> DNA



<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 29  
cgggtctacct gtatggcaac c

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<210> 30
<211> 22
<212> DNA
<213> Artificial Sequence
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<220> Description of Artificial Sequence: Synthetic  
<223> oligonucleotide probe

<400> 30  
gcaggacaac cagataaacc ac

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<210> 31
<211> 22
<212> DNA
<213> Artificial Sequence
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<220> Description of Artificial Sequence: Synthetic  
<223> oligonucleotide probe

<400> 31  
acgcagattt gagaaggctg tc

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<210> 32
<211> 46
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 32  
ttcacgggct gctcttgccc agctcttgaa gcttgaagag ctgcac

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<210> 33
<211> 3449
<212> DNA
<213> Homo sapiens
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<213> Homo sapiens
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cgctccccc gagcgatccc cgaggagagc cgcgggccctc ggcgaggcga agaggccgac 120

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 atgcaaaggt caaggagtcc atcgtggaca tcttgcaatt cttggacatt ggtcctgatg 480  
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 agggattccg gctcgtgag gatgggaaac gctgccgaag gaaggatgtc tgcaaatcaa 1920  
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 cagagggatt tgttctagct gaggacggaa gacggtgcaa gaaatgcact gaaggcccaa 2040  
 ttgacctggg ctttgtgatc gatggatcca agagtcttg agaagagaat tttgaggtcg 2100  
 tgaagcagtt tgtcactgga attatagatt ccttgacaat tcccccaaaa gccgctcag 2160  
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 acgtctccga gtgggcccag aaagccaagg ccaatgggat cactatgtat gctgttggg 2520  
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09909204 071004



ctgtagaaca ctggccatag gaaatgctgt ttttttgtac tggactttac cttgatatat 3360  
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<210> 34  
 <211> 915  
 <212> PRT  
 <213> Homo sapiens

<400> 34  
 Met Glu Lys Met Leu Ala Gly Cys Phe Leu Leu Ile Leu Gly Gln Ile 15  
 1 5 10  
 Val Leu Leu Pro Ala Glu Ala Arg Glu Arg Ser Arg Gly Arg Ser Ile 30  
 20 25 30  
 Ser Arg Gly Arg His Ala Arg Thr His Pro Gln Thr Ala Leu Leu Glu 45  
 35 40 45  
 Ser Ser Cys Glu Asn Lys Arg Ala Asp Leu Val Phe Ile Ile Asp Ser 60  
 50 55 60  
 Ser Arg Ser Val Asn Thr His Asp Tyr Ala Lys Val Lys Glu Phe Ile 80  
 65 70 75 80  
 Val Asp Ile Leu Gln Phe Leu Asp Ile Gly Pro Asp Val Thr Arg Val 95  
 85 90 95  
 Gly Leu Leu Gln Tyr Gly Ser Thr Val Lys Asn Glu Phe Ser Leu Lys 110  
 100 105 110  
 Thr Phe Lys Arg Lys Ser Glu Val Glu Arg Ala Val Lys Arg Met Arg 125  
 115 120 125  
 His Leu Ser Thr Gly Thr Met Thr Gly Leu Ala Ile Gln Tyr Ala Leu 140  
 130 135 140  
 Asn Ile Ala Phe Ser Glu Ala Glu Gly Ala Arg Pro Leu Arg Glu Asn 160  
 145 150 155 160  
 Val Pro Arg Val Ile Met Ile Val Thr Asp Gly Arg Pro Gln Asp Ser 175  
 165 170 175  
 Val Ala Glu Val Ala Ala Lys Ala Arg Asp Thr Gly Ile Leu Ile Phe 190  
 180 185 190  
 Ala Ile Gly Val Gly Gln Val Asp Phe Asn Thr Leu Lys Ser Ile Gly 205  
 195 200 205  
 Ser Glu Pro His Glu Asp His Val Phe Leu Val Ala Asn Phe Ser Gln 220  
 210 215 220  
 Ile Glu Thr Leu Thr Ser Val Phe Gln Lys Lys Leu Cys Thr Ala His

3449 3420 3360



225 230 235 240

Met Cys Ser Thr Leu Glu His Asn Cys Ala His Phe Cys Ile Asn Ile  
245 250 255

Pro Gly Ser Tyr Val Cys Arg Cys Lys Gln Gly Tyr Ile Leu Asn Ser  
260 265 270

Asp Gln Thr Thr Cys Arg Ile Gln Asp Leu Cys Ala Met Glu Asp His  
275 280 285

Asn Cys Glu Gln Leu Cys Val Asn Val Pro Gly Ser Phe Val Cys Gln  
290 295 300

Cys Tyr Ser Gly Tyr Ala Leu Ala Glu Asp Gly Lys Arg Cys Val Ala  
305 310 315 320

Val Asp Tyr Cys Ala Ser Glu Asn His Gly Cys Glu His Glu Cys Val  
325 330 335

Asn Ala Asp Gly Ser Tyr Leu Cys Gln Cys His Glu Gly Phe Ala Leu  
340 345 350

Asn Pro Asp Glu Lys Thr Cys Thr Arg Ile Asn Tyr Cys Ala Leu Asn  
355 360 365

Lys Pro Gly Cys Glu His Glu Cys Val Asn Met Glu Glu Ser Tyr Tyr  
370 375 380

Cys Arg Cys His Arg Gly Tyr Thr Leu Asp Pro Asn Gly Lys Thr Cys  
385 390 395 400

Ser Arg Val Asp His Cys Ala Gln Gln Asp His Gly Cys Glu Gln Leu  
405 410 415

Cys Leu Asn Thr Glu Asp Ser Phe Val Cys Gln Cys Ser Glu Gly Phe  
420 425 430

Leu Ile Asn Glu Asp Leu Lys Thr Cys Ser Arg Val Asp Tyr Cys Leu  
435 440 445

Leu Ser Asp His Gly Cys Glu Tyr Ser Cys Val Asn Met Asp Arg Ser  
450 455 460

Phe Ala Cys Gln Cys Pro Glu Gly His Val Leu Arg Ser Asp Gly Lys  
465 470 475 480

Thr Cys Ala Lys Leu Asp Ser Cys Ala Leu Gly Asp His Gly Cys Glu  
485 490 495

His Ser Cys Val Ser Ser Glu Asp Ser Phe Val Cys Gln Cys Phe Glu  
500 505 510



Gly Tyr Ile Leu Arg Glu Asp Gly Lys Thr Cys Arg Arg Lys Asp Val  
515 520 525

Cys Gln Ala Ile Asp His Gly Cys Glu His Ile Cys Val Asn Ser Asp  
530 535 540

Asp Ser Tyr Thr Cys Glu Cys Leu Glu Gly Phe Arg Leu Ala Glu Asp  
545 550 555 560

Gly Lys Arg Cys Arg Arg Lys Asp Val Cys Lys Ser Thr His His Gly  
565 570 575

Cys Glu His Ile Cys Val Asn Asn Gly Asn Ser Tyr Ile Cys Lys Cys  
580 585 590

Ser Glu Gly Phe Val Leu Ala Glu Asp Gly Arg Arg Cys Lys Lys Cys  
595 600 605

Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile Asp Gly Ser Lys Ser  
610 615 620

Leu Gly Glu Glu Asn Phe Glu Val Val Lys Gln Phe Val Thr Gly Ile  
625 630 635 640

Ile Asp Ser Leu Thr Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu  
645 650 655

Gln Tyr Ser Thr Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn  
660 665 670

Ser Ala Lys Asp Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly  
675 680 685

Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser  
690 695 700

Phe Thr Gln Gly Glu Gly Ala Arg Pro Leu Ser Thr Arg Val Pro Arg  
705 710 715 720

Ala Ala Ile Val Phe Thr Asp Gly Arg Ala Gln Asp Asp Val Ser Glu  
725 730 735

Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile Thr Met Tyr Ala Val Gly  
740 745 750

Val Gly Lys Ala Ile Glu Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro  
755 760 765

Thr Asn Lys His Leu Phe Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu  
770 775 780

Ile Ser Glu Lys Leu Lys Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser  
785 790 795 800



```
<210> 37
<211> 45
<212> DNA
<213> Artificial Sequence
```



45

<400> 37  
gcctgtcagt gtcctgaggg acacgtgctc cgcagcgatg ggaag

```
<210> 38
<211> 1813
<212> DNA
<213> Homo sapiens
```

<400> 38										
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cggcactgc	aggtccgtgc	gtcccgcggc	tggcgcccct	gactccgtcc	cgccagggga	120	ttgttcctgg	180		
gggccatgat	ttccctccc	gggccctgg	tgaccaactt	gctgcggtt	cccgccaacc	240	ttgcacgggg	300		
ggctgagtgc	cctcgcgccc	ccctcgcggg	cccagctgca	actgcacttg	aaacagaaag	360	cctggagtat	420		
ggttgcaggc	ggtgcaggga	ggggaagtgg	tgcttccagc	gtggtacacc	ctccaggaga	480	aaatctaggg	540		
aggtgtcttc	atcccagcca	tgggaggtgc	ccttttgtgat	gtggtctctc	ccatcctgcc	600	tctccaagga	660		
aaaaggagga	tcaggtgttg	tcctacatca	atggggctac	gctggagggt	actttctttg	720	tcttccatgg	780		
ccttggtcta	ctccatgcc	tcccggaacc	tgctccgtga	atgtgcaaga	tgccccaatgt	840	ggtagacctg	900		
aagactctgg	cccctacagc	tgtccctgcg	tactggttcc	tcagctcct	aaggccctgg	960	ccctggccca	1020		
gccacagcat	caaaacctta	gaactcaatg	acgtgaccct	gagctgccag	gcacgagccc	1080	agtctctcca	1140		
gtctccaggg	tgtgccccat	gtgggggcaa	ggcagcttcc	atccttccag	caaccaatat	1200	gtgcctgtga	1260		
gtaagccgc	tgtccaatac	cagtgggac	taagcctcac	caacctttcg	tgctctctta	1320	ctgagctatg	1380		
caccagcatt	agatgtcatc	cgtgggtctt	aggtgggcac	tgcccaatgt	tggtggggtt	1440	ctgtgggaaa	1500		
ctggagtcta	tgtctgcaag	ggagctgcag	tgggtgctgg	agctgttgtg	cccccaccac	1560	ctgaaattag	1620		
tgggaagtgag	cacagggcct	ggagctgcag	tgggtgctgg	agctgttgtg	tggtggggtt	1680	ctgtattgat	1740		
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aggagccagg	caatgatata	aaggaggatg	ccattgctcc	tgtcacctcc	tggtggggtt	1920	ataactgtc	1980		
agagctcaga	cacaatctcc	aagaatggga	ccctttctct	gtgcacctta	tggtggggtt	2040	ataactgtc	2100		
tccggccacc	ccatggccct	cccaggcctg	gtgcacctta	gtgcacctta	tggtggggtt	2160	ataactgtc	2220		
gccaggccct	gccctcacca	agactgcccc	cgacagatgg	ggccccaccct	tggtggggtt	2280	ataactgtc	2340		
cccccatccc	tggtggggtt	tcttctctct	tggtatgatg	acccaccac	tggtggggtt	2400	ataactgtc	2460		
tggtgcctgc	ccagagtcaa	gctggctctc	tcttataagg	gtcacctcta	tggtggggtt	2520	ataactgtc	2580		
aaggatttgg	ggtctctcct	cccttagtac	tctgccccca	tctgccccca	tggtggggtt	2640	ataactgtc	2700		
ggaaagagtc	acactcctga	gtgtccagga	gacagaagga	gaagaggaag	tggtggggtt	2760	ataactgtc	2820		
accatctcag	taagacctaa	acccctgact	cctccttatg	aagccagctg	tggtggggtt	2880	ataactgtc	2940		
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ctactcacca	agagtgaggg	aacaccaccc	ttggctcccc	ctccagctcc	tggtggggtt	3120	ataactgtc	3180		
tctgtacccc	acccctatct	gggttaggttt	tactggggca	gaggataggg	tggtggggtt	3240	ataactgtc	3300		
ataactgtc	aggctggctt	tggttaggttt	atttgcaaat	ttaaataaag	tggtggggtt	3360	ataactgtc	3420		
taaaactaac	atgaaatatg	tgttggtttt			tggtggggtt	3480	ataactgtc	3540		
tttgatatgaa	aaa				tggtggggtt	3600	ataactgtc	3660		

```
<210> 39
<211> 390
<212> PRT
<213> Homo sapiens
```

<400> 39  
Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu



1 5 10 15

Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln Leu Gln  
20 25 30

Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val  
35 40 45

Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln  
50 55 60

Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys  
65 70 75 80

Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro  
85 90 95

Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg  
100 105 110

Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val  
115 120 125

Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr  
130 135 140

Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu  
145 150 155 160

Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser  
165 170 175

Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro  
180 185 190

Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser  
195 200 205

Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys  
210 215 220

Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu  
225 230 235 240

Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly  
245 250 255

Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His  
260 265 270

Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp  
275 280 285



```
<210> 40
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
```

22

```
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
```

24

```
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
```



```
<210> 43
<211> 18
<212> DNA
<213> Artificial Sequence
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```
<400> 43                                     18
gtgtgacaca gcgtgggc
```

```
<210> 44
<211> 18
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 44 18  
gaccgggcagg cttctgcg

```
<210> 45
<211> 25
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 45 25  
cagcagcttc agccaccagg agtgg

```
<210> 46
<211> 24
<212> DNA
<213> Artificial Sequence
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```
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
```

```
<400> 46
ctgagccgtg ggctgcagtc tcgc
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<210> 47



<211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 47  
 ccgactacga ctggttcttc atcatgcagg atgacacata tgtgc

45

<210> 48  
 <211> 2822  
 <212> DNA  
 <213> Homo sapiens

<400> 48  
 cgccaccact gcggccaccg ccaatgaaac gctcccgcct cctagtgggtt ttttccactt 60  
 tggtgaattg ttctataact caaaattgca ccaagacacc ttgtctccca aatgcaaaat 120  
 gtgaaatagc caatggaatt gaagcctgct attgcaacat gggattttca ggaaatgggtg 180  
 tcacaatttg tgaagatgat aatgaatgtg gaaatttaac tcagtcctgt ggcgaaaatg 240  
 ctaattgcac taacacagaa ggaagttatt attgtatgtg tgtacctggc ttcagatcca 300  
 gcagtaacca agacagggtt atcactaatg atggaaccgt ctgtatagaa aatgtgaatg 360  
 caaactgcca tttagataat gtctgtatag ctgcaaatat taataaaaact ttaacaaaaa 420  
 tcagatccat aaaagaacct gtggctttgc tacaagaagt ctatagaaat tctgtgacag 480  
 atctttcacc aacagatata attacatata tagaaatatt agctgaatca tcttcattac 540  
 taggttacaa gaacaacact atctcagcca aggacaccct ttctaactca actcttactg 600  
 aatttgtaaa aaccgtgaat aattttgttc aaaggggatac atttgtagtt tgggacaagt 660  
 tatctgtgaa tcataggaga acacatctta caaaactcat gcacactgtt gaacaagcta 720  
 ctttaaggat atcccagagc ttccaaaaga ccacagagtt tgatacaaat tcaacggata 780  
 tagctctcaa agttttcttt tttgattcat ataacatgaa acatattcat cctcatatga 840  
 atatggatgg agactacata aatatatttc caaagagaaa agctgcatat gattcaaatg 900  
 gcaatgttgc agttgcattt ttatattata agagtattgg tcttttgctt tcatcatctg 960  
 acaacttctt attgaaacct caaaattatg ataattctga agaggaggaa agagtcatat 1020  
 cttcagtaat ttcagttctc atgagctcaa acccaccac attatatgaa cttgaaaaaa 1080  
 taacattttac attaagtcac cgaaagggtc cagataggtg taggagtcta tgtgcatttt 1140  
 ggaattactc acctgatacc atgaatggca gctggctctc agagggtgtg gagctgacat 1200  
 actcaaatga gaccacacc tcatgccgct gtaatcacct gacacatttt gcaattttga 1260  
 tgctctctgg tcttccattt ggtattaaag attataatat tcttacaagg atcactcaac 1320  
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 gtgaaattca aagcaccagg acaacaattc acaaaaatct ttgctgtagc ctatttcttg 1440  
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 ttgccggact gctacactac ttcttttttag ctgcttttgc atggatgtgc attgaaggca 1560  
 tacatctcta tctcattggt gtgggtgtca tctacaacaa gggatttttg cacaagaatt 1620  
 tttatatctt tggctatcta agcccagccg tggtagttgg attttcggca gcaactaggat 1680  
 acagatatta tggcacaacc aaagtatgtt ggcttagcac cgaaaacaac tttatttgga 1740  
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 tatacaagt ttttcgtcac actgcagggg tgaaaccaga agttagttgc tttgagaaca 1860  
 taaggtcttg tgcaagagga gccctcgctc ttctgttctt tctcggcacc acctggatct 1920  
 ttggggttct ccatgttgtg cacgcatcag tggttacagc ttacctcttc acagtcagca 1980  
 atgctttcca ggggatgttc atttttttat tcctgtgtgt tttatctaga aagattcaag 2040  
 aagaatatta cagattgttc aaaaatgtcc cctgttggtt tggatgttta aggtaaacat 2100  
 agagaatggg ggataattac aactgcacaa aaataaaaaat tccaagctgt ggatgaccaa 2160

HEPES 106065



```
<210> 49
<211> 690
<212> PRT
<213> Homo sapiens
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<400> 49  
Met Lys Arg Leu Pro Leu Leu Val Val Phe Ser Thr Leu Leu Asn Cys  
1 5 10 15  
Ser Tyr Thr Gln Asn Cys Thr Lys Thr Pro Cys Leu Pro Asn Ala Lys  
20 25 30  
Cys Glu Ile Arg Asn Gly Ile Glu Ala Cys Tyr Cys Asn Met Gly Phe  
35 40 45  
Ser Gly Asn Gly Val Thr Ile Cys Glu Asp Asp Asn Glu Cys Gly Asn  
50 55 60  
Leu Thr Gln Ser Cys Gly Glu Asn Ala Asn Cys Thr Asn Thr Glu Gly  
65 70 75 80  
Ser Tyr Tyr Cys Met Cys Val Pro Gly Phe Arg Ser Ser Ser Asn Gln  
85 90 95  
Asp Arg Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu Asn Val Asn  
100 105 110  
Ala Asn Cys His Leu Asp Asn Val Cys Ile Ala Ala Asn Ile Asn Lys  
115 120 125  
Thr Leu Thr Lys Ile Arg Ser Ile Lys Glu Pro Val Ala Leu Leu Gln  
130 135 140  
Glu Val Tyr Arg Asn Ser Val Thr Asp Leu Ser Pro Thr Asp Ile Ile  
145 150 155 160  
Thr Tyr Ile Glu Ile Leu Ala Glu Ser Ser Ser Leu Leu Gly Tyr Lys  
165 170 175  
Asn Asn Thr Ile Ser Ala Lys Asp Thr Leu Ser Asn Ser Thr Leu Thr



180 185 190

Glu Phe Val Lys Thr Val Asn Asn Phe Val Gln Arg Asp Thr Phe Val  
195 200 205

Val Trp Asp Lys Leu Ser Val Asn His Arg Arg Thr His Leu Thr Lys  
210 215 220

Leu Met His Thr Val Glu Gln Ala Thr Leu Arg Ile Ser Gln Ser Phe  
225 230 235 240

Gln Lys Thr Thr Glu Phe Asp Thr Asn Ser Thr Asp Ile Ala Leu Lys  
245 250 255

Val Phe Phe Phe Asp Ser Tyr Asn Met Lys His Ile His Pro His Met  
260 265 270

Asn Met Asp Gly Asp Tyr Ile Asn Ile Phe Pro Lys Arg Lys Ala Ala  
275 280 285

Tyr Asp Ser Asn Gly Asn Val Ala Val Ala Phe Leu Tyr Tyr Lys Ser  
290 295 300

Ile Gly Pro Leu Leu Ser Ser Ser Asp Asn Phe Leu Leu Lys Pro Gln  
305 310 315 320

Asn Tyr Asp Asn Ser Glu Glu Glu Glu Arg Val Ile Ser Ser Val Ile  
325 330 335

Ser Val Ser Met Ser Ser Asn Pro Pro Thr Leu Tyr Glu Leu Glu Lys  
340 345 350

Ile Thr Phe Thr Leu Ser His Arg Lys Val Thr Asp Arg Tyr Arg Ser  
355 360 365

Leu Cys Ala Phe Trp Asn Tyr Ser Pro Asp Thr Met Asn Gly Ser Trp  
370 375 380

Ser Ser Glu Gly Cys Glu Leu Thr Tyr Ser Asn Glu Thr His Thr Ser  
385 390 395 400

Cys Arg Cys Asn His Leu Thr His Phe Ala Ile Leu Met Ser Ser Gly  
405 410 415

Pro Ser Ile Gly Ile Lys Asp Tyr Asn Ile Leu Thr Arg Ile Thr Gln  
420 425 430

Leu Gly Ile Ile Ile Ser Leu Ile Cys Leu Ala Ile Cys Ile Phe Thr  
435 440 445

Phe Trp Phe Phe Ser Glu Ile Gln Ser Thr Arg Thr Thr Ile His Lys  
450 455 460



```
<210> 50
<211> 589
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (61)
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<223> a, t, c or g

<400> 50  
 tggaacata tcctccctca tatgaatatg gatggagact acataaatat atttccaaag 60  
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 gtattgggtcc ctttgctttc atcatctgac aacttcttat tgaaacctca aaattatgat 180  
 aattctgaag aggaggaaag agtcatatct tcagtaattt cagtctcaat gagctcaaac 240  
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 gataggata ggagtctatg tggcattttg gaatactcac ctgataccat gaatggcagc 360  
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 aatcacctga cacattttgc aattttgatg tcctctggtc cttccattgg tattaaagat 480  
 tataatattc ttacaaggat cactcaacta ggaataatta ttctactgat ttgtcttgcc 540  
 atatgcattt ttaccttctg gttcttcagt gaaattcaaa gcaccagga 589

<210> 51

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 51

ggtaatgagc tccattacag

20

<210> 52

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 52

ggagtagaaa gcgcatgg

18

<210> 53

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 53

cacctgatac catgaatggc ag

22

<210> 54

<211> 18

<212> DNA

090904-031504



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<400> 58
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<210> 59
<211> 216
<212> PRT
<213> Homo sapiens
```

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<400> 59  
Met Arg Ser Gly Cys Val Val Val His Val Trp Ile Leu Ala Gly Leu  
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Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro  
            20              25              30  
  
His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr  
        35              40              45  
  
Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala  
    50              55              60
```



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<210> 60
<211> 26
<212> DNA
<213> Artificial Sequence
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```
<400> 60
atccgcccag atggctacaa tgtgta
```

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<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
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<400> 61  
gcctcccggt ctccctgagc agtgccaaac agcggcagtg ta



<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

22

<400> 63						
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cccaaaagac	caacaagtag	tcacagcagt	agagtaccaa	gaggctattt	tagcctgcaa	240
aaccccaaa	aagactgttt	cctccagatt	agagtggaag	aaactgggtc	ggagtgtctc	300
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tttcaatata	cggatcaaaa	atgtgacaag	aagtgatgcy	gggaaatata	gttgtgaagt	420
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gctcacgcct	gtaatcccag	cactttggaa	ggccgcggcg	ggcggatcac	gaggtcagga	1020
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<210> 64
<211> 312
<212> PRT
<213> Homo sapiens
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<400> 64  
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20 25 30



Lys Asp Gln Gln Val Val Thr Ala Val Glu Tyr Gln Glu Ala Ile Leu  
35 40 45

Ala Cys Lys Thr Pro Lys Lys Thr Val Ser Ser Arg Leu Glu Trp Lys  
50 55 60

Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr Gln Gln Thr Leu Gln  
65 70 75 80

Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile  
85 90 95

Lys Asn Val Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser  
100 105 110

Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu  
115 120 125

Glu Val Leu Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser  
130 135 140

Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly  
145 150 155 160

Asn Pro Ala Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu  
165 170 175

Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met  
180 185 190

Asn Thr Lys Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp  
195 200 205

Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg  
210 215 220

Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile  
225 230 235 240

Ile Ala Ala Val Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu  
245 250 255

Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser  
260 265 270

Phe Gln Lys Ser Asn Ser Ser Ser Lys Ala Thr Thr Met Ser Glu Asn  
275 280 285

Val Gln Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Lys Ala Ala Ala  
290 295 300

Gly Gly Ser Arg Gly Gln Glu Phe



310

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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<210> 66
<211> 23
<212> DNA
<213> Artificial Sequence
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<400> 66 23  
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 67  
qqaagaggat acagtcactc tggaagtatt agtggctcca gcagttcc 48

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<210> 68
<211> 2639
<212> DNA
<213> Homo sapiens
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[illegible]



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 aaaacaattt atcttcagtc accaatatta atgtaaaaaa gatgcctcag ctcctttctg 840  
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<210> 69

<211> 708

<212> PRT

<213> Homo sapiens

<400> 69

Met Lys Asp Met Pro Leu Arg Ile His Val Leu Leu Gly Leu Ala Ile  
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Thr Thr Leu Val Gln Ala Val Asp Lys Lys Val Asp Cys Pro Arg Leu  
 20 25 30

Cys Thr Cys Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser Ile Tyr Met  
 35 40 45

Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro  
 50 55 60



Ala Arg Leu Pro Ala Asn Thr Gln Ile Leu Leu Leu Gln Thr Asn Asn  
65 70 75 80

Ile Ala Lys Ile Glu Tyr Ser Thr Asp Phe Pro Val Asn Leu Thr Gly  
85 90 95

Leu Asp Leu Ser Gln Asn Asn Leu Ser Ser Val Thr Asn Ile Asn Val  
100 105 110

Lys Lys Met Pro Gln Leu Leu Ser Val Tyr Leu Glu Glu Asn Lys Leu  
115 120 125

Thr Glu Leu Pro Glu Lys Cys Leu Ser Glu Leu Ser Asn Leu Gln Glu  
130 135 140

Leu Tyr Ile Asn His Asn Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe  
145 150 155 160

Ile Gly Leu His Asn Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu  
165 170 175

Gln Met Ile Asn Ser Lys Trp Phe Asp Ala Leu Pro Asn Leu Glu Ile  
180 185 190

Leu Met Ile Gly Glu Asn Pro Ile Ile Arg Ile Lys Asp Met Asn Phe  
195 200 205

Lys Pro Leu Ile Asn Leu Arg Ser Leu Val Ile Ala Gly Ile Asn Leu  
210 215 220

Thr Glu Ile Pro Asp Asn Ala Leu Val Gly Leu Glu Asn Leu Glu Ser  
225 230 235 240

Ile Ser Phe Tyr Asp Asn Arg Leu Ile Lys Val Pro His Val Ala Leu  
245 250 255

Gln Lys Val Val Asn Leu Lys Phe Leu Asp Leu Asn Lys Asn Pro Ile  
260 265 270

Asn Arg Ile Arg Arg Gly Asp Phe Ser Asn Met Leu His Leu Lys Glu  
275 280 285

Leu Gly Ile Asn Asn Met Pro Glu Leu Ile Ser Ile Asp Ser Leu Ala  
290 295 300

Val Asp Asn Leu Pro Asp Leu Arg Lys Ile Glu Ala Thr Asn Asn Pro  
305 310 315 320

Arg Leu Ser Tyr Ile His Pro Asn Ala Phe Phe Arg Leu Pro Lys Leu  
325 330 335

Glu Ser Leu Met Leu Asn Ser Asn Ala Leu Ser Ala Leu Tyr His Gly



340 345 350

Thr Ile Glu Ser Leu Pro Asn Leu Lys Glu Ile Ser Ile His Ser Asn  
355 360 365

Pro Ile Arg Cys Asp Cys Val Ile Arg Trp Met Asn Met Asn Lys Thr  
370 375 380

Asn Ile Arg Phe Met Glu Pro Asp Ser Leu Phe Cys Val Asp Pro Pro  
385 390 395 400

Glu Phe Gln Gly Gln Asn Val Arg Gln Val His Phe Arg Asp Met Met  
405 410 415

Glu Ile Cys Leu Pro Leu Ile Ala Pro Glu Ser Phe Pro Ser Asn Leu  
420 425 430

Asn Val Glu Ala Gly Ser Tyr Val Ser Phe His Cys Arg Ala Thr Ala  
435 440 445

Glu Pro Gln Pro Glu Ile Tyr Trp Ile Thr Pro Ser Gly Gln Lys Leu  
450 455 460

Leu Pro Asn Thr Leu Thr Asp Lys Phe Tyr Val His Ser Glu Gly Thr  
465 470 475 480

Leu Asp Ile Asn Gly Val Thr Pro Lys Glu Gly Gly Leu Tyr Thr Cys  
485 490 495

Ile Ala Thr Asn Leu Val Gly Ala Asp Leu Lys Ser Val Met Ile Lys  
500 505 510

Val Asp Gly Ser Phe Pro Gln Asp Asn Asn Gly Ser Leu Asn Ile Lys  
515 520 525

Ile Arg Asp Ile Gln Ala Asn Ser Val Leu Val Ser Trp Lys Ala Ser  
530 535 540

Ser Lys Ile Leu Lys Ser Ser Val Lys Trp Thr Ala Phe Val Lys Thr  
545 550 555 560

Glu Asn Ser His Ala Ala Gln Ser Ala Arg Ile Pro Ser Asp Val Lys  
565 570 575

Val Tyr Asn Leu Thr His Leu Asn Pro Ser Thr Glu Tyr Lys Ile Cys  
580 585 590

Ile Asp Ile Pro Thr Ile Tyr Gln Lys Asn Arg Lys Lys Cys Val Asn  
595 600 605

Val Thr Thr Lys Gly Leu His Pro Asp Gln Lys Glu Tyr Glu Lys Asn  
610 615 620



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<210> 70
<211> 1305
<212> DNA
<213> Homo sapiens
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<210> 71
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<212> PRT
<213> Homo sapiens
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 20 25 30  
 Met Cys Pro Lys Gly Cys Leu Cys Ser Ser Ser Gly Gly Leu Asn Val  
 35 40 45  
 Thr Cys Ser Asn Ala Asn Leu Lys Glu Ile Pro Arg Asp Leu Pro Pro  
 50 55 60  
 Glu Thr Val Leu Leu Tyr Leu Asp Ser Asn Gln Ile Thr Ser Ile Pro  
 65 70 75 80  
 Asn Glu Ile Phe Lys Asp Leu His Gln Leu Arg Val Leu Asn Leu Ser  
 85 90 95  
 Lys Asn Gly Ile Glu Phe Ile Asp Glu His Ala Phe Lys Gly Val Ala  
 100 105 110  
 Glu Thr Leu Gln Thr Leu Asp Leu Ser Asp Asn Arg Ile Gln Ser Val  
 115 120 125  
 His Lys Asn Ala Phe Asn Asn Leu Lys Ala Arg Ala Arg Ile Ala Asn  
 130 135 140  
 Asn Pro Trp His Cys Asp Cys Thr Leu Gln Gln Val Leu Arg Ser Met  
 145 150 155 160  
 Ala Ser Asn His Glu Thr Ala His Asn Val Ile Cys Lys Thr Ser Val  
 165 170 175  
 Leu Asp Glu His Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala  
 180 185 190  
 Asp Leu Cys Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val  
 195 200 205  
 Thr Met Phe Gly Trp Phe Thr Met Val Ile Ser Tyr Val Val Tyr Tyr  
 210 215 220  
 Val Arg Gln Asn Gln Glu Asp Ala Arg Arg His Leu Glu Tyr Leu Lys  
 225 230 235 240  
 Ser Leu Pro Ser Arg Gln Lys Lys Ala Asp Glu Pro Asp Asp Ile Ser  
 245 250 255  
 Thr Val Val

&lt;210&gt; 72

&lt;211&gt; 2290

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&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 72

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aaaaaaaaa

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&lt;210&gt; 73

&lt;211&gt; 620

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 73

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Met Gln Val Ser Lys Arg Met Leu Ala Gly Gly Val Arg Ser Met Pro
1           5           10           15

```



Ser Pro Leu Leu Ala Cys Trp Gln Pro Ile Leu Leu Leu Val Leu Gly  
20 25 30

Ser Val Leu Ser Gly Ser Ala Thr Gly Cys Pro Pro Arg Cys Glu Cys  
35 40 45

Ser Ala Gln Asp Arg Ala Val Leu Cys His Arg Lys Cys Phe Val Ala  
50 55 60

Val Pro Glu Gly Ile Pro Thr Glu Thr Arg Leu Leu Asp Leu Gly Lys  
65 70 75 80

Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu Phe Ala Ser Phe Pro His  
85 90 95

Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile Val Ser Ala Val Glu Pro  
100 105 110

Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg Thr Leu Gly Leu Arg Ser  
115 120 125

Asn Arg Leu Lys Leu Ile Pro Leu Gly Val Phe Thr Gly Leu Ser Asn  
130 135 140

Leu Thr Lys Gln Asp Ile Ser Glu Asn Lys Ile Val Ile Leu Leu Asp  
145 150 155 160

Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys Ser Leu Glu Val Gly Asp  
165 170 175

Asn Asp Leu Val Tyr Ile Ser His Arg Ala Phe Ser Gly Leu Asn Ser  
180 185 190

Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr Ser Ile Pro Thr  
195 200 205

Glu Ala Leu Ser His Leu His Gly Leu Ile Val Leu Arg Leu Arg His  
210 215 220

Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser Phe Lys Arg Leu Tyr Arg  
225 230 235 240

Leu Lys Val Leu Glu Ile Ser His Trp Pro Tyr Leu Asp Thr Met Thr  
245 250 255

Pro Asn Cys Leu Tyr Gly Leu Asn Leu Thr Ser Leu Ser Ile Thr His  
260 265 270

Cys Asn Leu Thr Ala Val Pro Tyr Leu Ala Val Arg His Leu Val Tyr  
275 280 285

Leu Arg Phe Leu Asn Leu Ser Tyr Asn Pro Ile Ser Thr Ile Glu Gly  
290 295 300



Ser Met Leu His Glu Leu Leu Arg Leu Gln Glu Ile Gln Leu Val Gly 320  
305 310 315

Gly Gln Leu Ala Val Val Glu Pro Tyr Ala Phe Arg Gly Leu Asn Tyr 335  
325 330

Leu Arg Val Leu Asn Val Ser Gly Asn Gln Leu Thr Thr Leu Glu Glu 350  
340 345

Ser Val Phe His Ser Val Gly Asn Leu Glu Thr Leu Ile Leu Asp Ser 365  
355 360

Asn Pro Leu Ala Cys Asp Cys Arg Leu Leu Trp Val Phe Arg Arg Arg 380  
370 375

Trp Arg Leu Asn Phe Asn Arg Gln Gln Pro Thr Cys Ala Thr Pro Glu 400  
385 390 395

Phe Val Gln Gly Lys Glu Phe Lys Asp Phe Pro Asp Val Leu Leu Pro 415  
405 410

Asn Tyr Phe Thr Cys Arg Arg Ala Arg Ile Arg Asp Arg Lys Ala Gln 430  
420 425

Gln Val Phe Val Asp Glu Gly His Thr Val Gln Phe Val Cys Arg Ala 445  
435 440

Asp Gly Asp Pro Pro Pro Ala Ile Leu Trp Leu Ser Pro Arg Lys His 460  
450 455

Leu Val Ser Ala Lys Ser Asn Gly Arg Leu Thr Val Phe Pro Asp Gly 480  
465 470 475

Thr Leu Glu Val Arg Tyr Ala Gln Val Gln Asp Asn Gly Thr Tyr Leu 495  
485 490

Cys Ile Ala Ala Asn Ala Gly Gly Asn Asp Ser Met Pro Ala His Leu 510  
500 505

His Val Arg Ser Tyr Ser Pro Asp Trp Pro His Gln Pro Asn Lys Thr 525  
515 520

Phe Ala Phe Ile Ser Asn Gln Pro Gly Glu Gly Glu Ala Asn Ser Thr 540  
530 535

Arg Ala Thr Val Pro Phe Pro Phe Asp Ile Lys Thr Leu Ile Ile Ala 560  
545 550 555

Thr Thr Met Gly Phe Ile Ser Phe Leu Gly Val Val Leu Phe Cys Leu 575  
565 570

Val Leu Leu Phe Leu Trp Ser Arg Gly Lys Gly Asn Thr Lys His Asn



Ala Asp Ala Pro Arg Lys Phe Asn Met Lys Met Ile  
610 615 620

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<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

22

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<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

23

<220>  
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oligonucleotide probe

50  
52

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oligonucleotide probe



22

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<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
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23

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<220>
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        oligonucleotide probe
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50

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<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
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22

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      oligonucleotide probe
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24

<210> 82



<211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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 oligonucleotide probe

<400> 82  
 gactacatgt ttcaggacct gtacaacctc aagtcactgg aggttggcga 50

<210> 83  
 <211> 1685  
 <212> DNA  
 <213> Homo sapiens

<400> 83  
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 agccaggag cggccggga agcgcgatgg gggccccagc cgcctcgctc ctgctcctgc 180  
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 agctcagcat cagcatcagc aatgtggccc tggcagacga gggcgagtac acctgctcaa 480  
 tcttcactat gcctgtgcga actgccaagt ccctcgtcac tgtgctagga attccacaga 540  
 agcccatcat cactgggtat aaatcttcat tacgggaaaa agacacagcc accctaaact 600  
 gtcagtcttc tgggagcaag cctgcagccc ggctcacctg gagaaagggt gaccaagaac 660  
 tccacggaga accaaccgac atacaggaag atcccaatgg taaaaccttc actgtcagca 720  
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 ctcccgttg ctcccagcc caccacccc cctgtacaga atgtctgctt tgggtgcggg 1500  
 tttgtactcg gtttggaatg gggaggagg agggcgggg gaggggaggg ttgacctcag 1560  
 ccctttccgt ggcttctctg catttggtt attattatt ttgtaacaat cccaaatcaa 1620  
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 aaaca 1685

<210> 84  
 <211> 398  
 <212> PRT  
 <213> Homo sapiens

<400> 84

1026660



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 20 25 30  
 Pro Trp Thr Ser Asp Glu Thr Val Val Ala Gly Gly Thr Val Val Leu  
 35 40 45  
 Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Asn  
 50 55 60  
 Pro Ala Gln Gln Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp  
 65 70 75 80  
 Asn Arg Ile Gln Leu Val Thr Ser Thr Pro His Glu Leu Ser Ile Ser  
 85 90 95  
 Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile  
 100 105 110  
 Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu Val Thr Val Leu Gly  
 115 120 125  
 Ile Pro Gln Lys Pro Ile Ile Thr Gly Tyr Lys Ser Ser Leu Arg Glu  
 130 135 140  
 Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser Gly Ser Lys Pro Ala  
 145 150 155 160  
 Ala Arg Leu Thr Trp Arg Lys Gly Asp Gln Glu Leu His Gly Glu Pro  
 165 170 175  
 Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr Phe Thr Val Ser Ser  
 180 185 190  
 Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp Gly Ala Ser Ile Val  
 195 200 205  
 Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser  
 210 215 220  
 Gln Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp  
 225 230 235 240  
 Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu Leu His Cys Glu Gly  
 245 250 255  
 Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu Gly Ser  
 260 265 270  
 Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala Leu Ile Phe Pro Phe  
 275 280 285

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Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn  
 290 295 300

Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser  
 305 310 315 320

Pro Val Pro Ser Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile  
 325 330 335

Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly  
 340 345 350

His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys  
 355 360 365

Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu  
 370 375 380

Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile  
 385 390 395

<210> 85

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 85

gctaggaatt ccacagaagc cc

22

<210> 86

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 86

aacctggaat gtcaccgagc tg

22

<210> 87

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

TOP201026660



## oligonucleotide probe

<400> 87  
 cctagcacag tgacgagggga cttggc 26

<210> 88  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 88  
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<210> 89  
 <211> 50  
 <212> DNA  
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 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 89  
 gccctggcag acgagggcga gtacacctgc tcaatcttca ctatgcctgt 50

<210> 90  
 <211> 2755  
 <212> DNA  
 <213> Homo sapiens

<400> 90  
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 gctgttactt tgtgatgaga tcggggatga attgctcgct ttaaaaaatgc tgctttggat 180  
 tctgttgctg gagacgtctc tttgttttgc cgctggaaac gttacagggg acgtttgcaa 240  
 agagaagatc tgttcctgca atgagataga aggggaccta cacgtagact gtgaaaaaaaa 300  
 gggcttcaca agtctgcagc gtttcactgc cccgacttcc cagttttacc atttatttct 360  
 gcatggcaat tccctcactc gacttttccc taatgagttc gctaactttt ataatgcggt 420  
 tagtttgac atggaaaaca atggccttgc tgaaatcggt ccgggggctt ttctggggct 480  
 gcagctggtg aaaaggctgc acatcaacaa caacaagatc aagtcttttc gaaagcagac 540  
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 agacccgggg gccttccagg acttgaacaa gctggagggtg ctcatatttaa atgacaatct 660  
 catcagcacc ctacctgcca acgtgttcca gtatgtgccc atcaccacc tgcacctccg 720  
 gggtaacagg ctgaaaacgc tgccctatga ggaggctctg gagcaaatcc ctggtattgc 780  
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 cagactgcag ggtaaagacc tcaatgaaac caccgaacag gacttgtgtc ctttgaaaaa 960  
 ccgagtggat tctagtctcc cggcgcccc tgcccaagaa gagaccttg ctctgggacc 1020  
 cctgccaaact cctttcaaga caaatgggca agaggatcat gccacaccag ggtctgctcc 1080

F0042043660



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<210> 91
<211> 696
<212> PRT
<213> Homo sapiens
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Glu Ile Glu Gly Asp Leu His Val Asp Cys Glu Lys Lys Gly Phe Thr  
35 40 45  
Ser Leu Gln Arg Phe Thr Ala Pro Thr Ser Gln Phe Tyr His Leu Phe  
50 55 60  
Leu His Gly Asn Ser Leu Thr Arg Leu Phe Pro Asn Glu Phe Ala Asn  
65 70 75 80  
Phe Tyr Asn Ala Val Ser Leu His Met Glu Asn Asn Gly Leu His Glu  
85 90 95



Ile Val Pro Gly Ala Phe Leu Gly Leu Gln Leu Val Lys Arg Leu His  
100 105 110

Ile Asn Asn Asn Lys Ile Lys Ser Phe Arg Lys Gln Thr Phe Leu Gly  
115 120 125

Leu Asp Asp Leu Glu Tyr Leu Gln Ala Asp Phe Asn Leu Leu Arg Asp  
130 135 140

Ile Asp Pro Gly Ala Phe Gln Asp Leu Asn Lys Leu Glu Val Leu Ile  
145 150 155 160

Leu Asn Asp Asn Leu Ile Ser Thr Leu Pro Ala Asn Val Phe Gln Tyr  
165 170 175

Val Pro Ile Thr His Leu Asp Leu Arg Gly Asn Arg Leu Lys Thr Leu  
180 185 190

Pro Tyr Glu Glu Val Leu Glu Gln Ile Pro Gly Ile Ala Glu Ile Leu  
195 200 205

Leu Glu Asp Asn Pro Trp Asp Cys Thr Cys Asp Leu Leu Ser Leu Lys  
210 215 220

Glu Trp Leu Glu Asn Ile Pro Lys Asn Ala Leu Ile Gly Arg Val Val  
225 230 235 240

Cys Glu Ala Pro Thr Arg Leu Gln Gly Lys Asp Leu Asn Glu Thr Thr  
245 250 255

Glu Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser Leu Pro  
260 265 270

Ala Pro Pro Ala Gln Glu Glu Thr Phe Ala Pro Gly Pro Leu Pro Thr  
275 280 285

Pro Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr Pro Gly Ser Ala  
290 295 300

Pro Asn Gly Gly Thr Lys Ile Pro Gly Asn Trp Gln Ile Lys Ile Arg  
305 310 315 320

Pro Thr Ala Ala Ile Ala Thr Gly Ser Ser Arg Asn Lys Pro Leu Ala  
325 330 335

Asn Ser Leu Pro Cys Pro Gly Gly Cys Ser Cys Asp His Ile Pro Gly  
340 345 350

Ser Gly Leu Lys Met Asn Cys Asn Asn Arg Asn Val Ser Ser Leu Ala  
355 360 365

Asp Leu Lys Pro Lys Leu Ser Asn Val Gln Glu Leu Phe Leu Arg Asp  
370 375 380



Asn Lys Ile His Ser Ile Arg Lys Ser His Phe Val Asp Tyr Lys Asn  
385 390 395 400

Leu Ile Leu Leu Asp Leu Gly Asn Asn Asn Ile Ala Thr Val Glu Asn  
405 410 415

Asn Thr Phe Lys Asn Leu Leu Asp Leu Arg Trp Leu Tyr Met Asp Ser  
420 425 430

Asn Tyr Leu Asp Thr Leu Ser Arg Glu Lys Phe Ala Gly Leu Gln Asn  
435 440 445

Leu Glu Tyr Leu Asn Val Glu Tyr Asn Ala Ile Gln Leu Ile Leu Pro  
450 455 460

Gly Thr Phe Asn Ala Met Pro Lys Leu Arg Ile Leu Ile Leu Asn Asn  
465 470 475 480

Asn Leu Leu Arg Ser Leu Pro Val Asp Val Phe Ala Gly Val Ser Leu  
485 490 495

Ser Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro Val Ala  
500 505 510

Gly Val Leu Asp Gln Leu Thr Ser Ile Ile Gln Ile Asp Leu His Gly  
515 520 525

Asn Pro Trp Glu Cys Ser Cys Thr Ile Val Pro Phe Lys Gln Trp Ala  
530 535 540

Glu Arg Leu Gly Ser Glu Val Leu Met Ser Asp Leu Lys Cys Glu Thr  
545 550 555 560

Pro Val Asn Phe Phe Arg Lys Asp Phe Met Leu Leu Ser Asn Asp Glu  
565 570 575

Ile Cys Pro Gln Leu Tyr Ala Arg Ile Ser Pro Thr Leu Thr Ser His  
580 585 590

Ser Lys Asn Ser Thr Gly Leu Ala Glu Thr Gly Thr His Ser Asn Ser  
595 600 605

Tyr Leu Asp Thr Ser Arg Val Ser Ile Ser Val Leu Val Pro Gly Leu  
610 615 620

Leu Leu Val Phe Val Thr Ser Ala Phe Thr Val Val Gly Met Leu Val  
625 630 635 640

Phe Ile Leu Arg Asn Arg Lys Arg Ser Lys Arg Arg Asp Ala Asn Ser  
645 650 655

Ser Ala Ser Glu Ile Asn Ser Leu Gln Thr Val Cys Asp Ser Ser Tyr



660 665 670  
 Trp His Asn Gly Pro Tyr Asn Ala Asp Gly Ala His Arg Val Tyr Asp  
 675 680 685

Cys Gly Ser His Ser Leu Ser Asp  
 690 695

<210> 92  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 92  
 gttggatctg ggcaacaata ac

22

<210> 93  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 93  
 attggtgtgc aggctgagtt taag

24

<210> 94  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 94  
 ggtggctata catggatagc aattacctgg acacgctgtc ccggg

45

<210> 95  
 <211> 2226  
 <212> DNA  
 <213> Homo sapiens

<400> 95  
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0990904 0704



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 <211> 490  
 <212> PRT  
 <213> Homo sapiens

<400> 96  
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 Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln  
 35 40 45  
 Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val  
 50 55 60



Arg Ala Gly Ala Glu Leu Arg Ala Val Leu Ala Leu Leu Arg Ala Gly  
65 70 75 80

Pro Gly Pro Gly Gly Gly Ser Lys Asp Leu Leu Phe Trp Val Ala Leu  
85 90 95

Glu Arg Arg Arg Ser His Cys Thr Leu Glu Asn Glu Pro Leu Arg Gly  
100 105 110

Phe Ser Trp Leu Ser Ser Asp Pro Gly Gly Leu Glu Ser Asp Thr Leu  
115 120 125

Gln Trp Val Glu Glu Pro Gln Arg Ser Cys Thr Ala Arg Arg Cys Ala  
130 135 140

Val Leu Gln Ala Thr Gly Gly Val Glu Pro Ala Gly Trp Lys Glu Met  
145 150 155 160

Arg Cys His Leu Arg Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu  
165 170 175

Val Leu Cys Pro Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr  
180 185 190

Arg Ala Pro Phe Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro  
195 200 205

Gly Thr Glu Val Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val  
210 215 220

Thr Cys Ile Ala Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly  
225 230 235 240

Asp Val Leu Cys Pro Cys Pro Gly Arg Tyr Leu Arg Ala Gly Lys Cys  
245 250 255

Ala Glu Leu Pro Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala Cys Glu  
260 265 270

Cys Ala Thr Gly Phe Glu Leu Gly Lys Asp Gly Arg Ser Cys Val Thr  
275 280 285

Ser Gly Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg  
290 295 300

Arg Pro Pro Ala Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro  
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Ile Arg Val Asp Glu Lys Leu Gly Glu Thr Pro Leu Val Pro Glu Gln  
325 330 335

Asp Asn Ser Val Thr Ser Ile Pro Glu Ile Pro Arg Trp Gly Ser Gln



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<210> 97
<211> 24
<212> DNA
<213> Artificial Sequence
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<400> 97  
tggaaggaga tgcgatgccca cctg

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<210> 98
<211> 20
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 98  
tgaccagtgg ggaaggacag



<211> DNA  
<212> DNA  
<213> Artificial Sequence

20

<210> 100  
<211> 24  
<212> DNA  
<213> Artificial Sequence

24

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<210> 101
<211> 24
<212> DNA
<213> Artificial Sequence
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24

```
<210> 102
<211> 50
<212> DNA
<213> Artificial Sequence
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50

```
<210> 103
<211> 2026
<212> DNA
<213> Homo sapiens
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GGGCGCGG  
TGTCTGCT

<400> 103  
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 agcgtcgagt cagacggcac cataatcgcc tttaaaagtg cctccgccct gccggccgcg 120  
 tatcccccg ctacctgggc cgcccccgcg cgggtgcgcgc gtgagagggg gcgcgcggcg 180  
 agccgagcgc cgggtgtgagc cagcgtgctt gccagtgtga gcggcggtgt gagcgtctac 240  
 ggtgcggagg ggcgtgtgtg ccggcgcgcg cggcgtgggg tgctgtggc tgcgccacc 360  
 gctgccatga ggggcgcgaa ccagagaga cctgttttca catgtggtgg cattctact 420  
 cagctctcgc ggcagcagtc cccagagaga tttcctggag tgtaccctcc aaatagcaaa 480  
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 tgtacttga aaatcacagt tcccgaagga gactttgtgg ctggagccct tgtgtccatg 600  
 gacctcgaga gtgacaacct gtgccgctat actttccggc agctggcaa tggcttcagt 660  
 aatggccagc gcattggcgc cttctgtggc gatgccaaca cagctggcaa aggactcctt 720  
 ggcaacaaga tgatggtgca gatgatttct agaggggatc agtattgtgg aggactcctt 780  
 gccatgttct ccgctgctga accaaacgaa agaggggatc accgggatta ccctgcagga 840  
 gacagacctt ccggtcttct taaaaccccc aactggccag accgggatta aaagtttgag 900  
 gtcacttgtg tgtggcacat tgtagccca aagaatcagc ttatagaatt aaagtttgag 960  
 aagtttgatg tggagcgaga taactactgc cgaatgatt atgtggtgt gtttaattggc 1020  
 ggggaagtca acgatgctag aagaattgga aagtattgt gtgtagtcc acctgcgcca 1080  
 attgtgtctg agagaaatga acttcttatt cagttttat cagacttaag ttttaactgca 1140  
 gatgggttta ttggctacta catattcagg ggtttaaaac ccaccgtggc cttgtgtcaa 1200  
 cctgtcacca ccacattccc tgtaaccacg ggtttaaaac ccaccgtggc cttgtgtcaa 1260  
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 gccggcactg ttatcacaaac catcactcgc gatgggagtt tgcacgccac catgagtgc 1380  
 atcaacatct acaagaggg aaatttggcg attcagcagg cgggcaagaa catgagtgc 1440  
 aggtgactg tctgtgcaa gcagtgcctt cctctcagaa gaggtctaaa ttacattatt 1500  
 atgggccaag taggtgaaga tgggcgaggg gccttaaaaa ataagcaatg ttaacagtga 1560  
 ttcaagacca agaatcagaa gctcctggat tgcctttgaa agatctatgt tctctcagta 1620  
 actgtgtcca tttaagctgt attctgcat ctgaaagagg attccgaaa agtggtactg 1680  
 gaaaaaaaaa tacttataaa attacatatt ctccgagata gctgagggaa gttctttgcc 1740  
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 ctaaaagtgt caagcgttga cagcttgga gcgtttatt atacatctct gtaaaaggat 1920  
 attttagaat tgagttgtg gaagatgtca aaaaaagatt ttagaagtc aatatttata 1980  
 gtgtatttg tttcaccttc aagcctttgc cctgaggtgt tacaatctg tcttgcgttt 2026  
 tctaatcaa tgcttaataa aatattttta aaggaaaaaa aaaaaa

<210> 104  
 <211> 415  
 <212> PRT  
 <213> Homo sapiens

<400> 104  
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 1 5 10  
 Ala Thr Gln Leu Ser Arg Gln Gln Ser Pro Glu Arg Pro Val Phe Thr 30  
 20 25 30  
 Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly 45  
 35 40 45  
 Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr 60  
 50 55 60



Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu 80  
65 70 75

Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly 95  
85 90

His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro 110  
100 105

Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser 125  
115 120

Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala 140  
130 135

Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg 160  
145 150 155

Pro Ser Gly Ser Phe Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro 175  
165 170

Ala Gly Val Thr Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu 190  
180 185

Ile Glu Leu Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys 205  
195 200

Arg Tyr Asp Tyr Val Ala Val Phe Asn Gly Gly Glu Val Asn Asp Ala 220  
210 215

Arg Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val 240  
225 230 235

Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu 255  
245 250

Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu 270  
260 265

Pro Thr Thr Thr Glu Gln Pro Val Thr Thr Thr Phe Pro Val Thr Thr 285  
275 280

Gly Leu Lys Pro Thr Val Ala Leu Cys Gln Gln Lys Cys Arg Arg Thr 300  
290 295

Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp Phe Val Leu Ala Gly 320  
305 310 315

Thr Val Ile Thr Thr Ile Thr Arg Asp Gly Ser Leu His Ala Thr Val 335  
325 330

Ser Ile Ile Asn Ile Tyr Lys Glu Gly Asn Leu Ala Ile Gln Gln Ala



340 345 350  
 Gly Lys Asn Met Ser Ala Arg Leu Thr Val Val Cys Lys Gln Cys Pro  
 355 360 365  
 Leu Leu Arg Arg Gly Leu Asn Tyr Ile Ile Met Gly Gln Val Gly Glu  
 370 375 380  
 Asp Gly Arg Gly Lys Ile Met Pro Asn Ser Phe Ile Met Met Phe Lys  
 385 390 395 400  
 Thr Lys Asn Gln Lys Leu Leu Asp Ala Leu Lys Asn Lys Gln Cys  
 405 410 415

<210> 105  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

22

<400> 105  
 ccgattcata gacctcgaga gt

<210> 106  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

22

<400> 106  
 gtcaaggagt cctccacaat ac

<210> 107  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

45

<400> 107  
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<210> 108  
 <211> 1838  
 <212> DNA

T00100000000



&lt;213&gt; Homo sapiens

&lt;400&gt; 108

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aagggcctag tcccagctgt gctctggggc ctcagcctct tctcaacct cccaggacct 180
atctggctcc agccctctcc acctccccag tcttctcccc cgcctcagcc ccatccgtgt 240
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aactttggag gtggaaacac tgccctgggag gaagagaatt tgtccaaata caaagacagt 360
gagacccgcc tggtagaggt gctggagggt gtgtgcagca agtcagactt cgagtggccac 420
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gcccaggtag ccaggccccg gcagacaagg ccctgggggt aaaaagtagc cctgaagggtg 1560
gataccatga gctcttcacc tggcggggac tggcaggctt cacaatgtgt gaatttcaaa 1620
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acaggggtgg ggccatcaca gctccctcct gccagctgca tgetgccagt tctgttctg 1740
tgttcaccac atccccacac cccattgcc cttatttatt catctcagga aataaagaaa 1800
ggtcttggaa agttaaaaaa aaaaaaaaaa aaaaaaaaaa 1838

```

&lt;210&gt; 109

&lt;211&gt; 420

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 109

```

Met Ala Pro Trp Pro Pro Lys Gly Leu Val Pro Ala Val Leu Trp Gly
  1              5              10              15

Leu Ser Leu Phe Leu Asn Leu Pro Gly Pro Ile Trp Leu Gln Pro Ser
      20              25              30

Pro Pro Pro Gln Ser Ser Pro Pro Pro Gln Pro His Pro Cys His Thr
      35              40              45

Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile
      50              55              60

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F002043666



Arg Asp Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Glu Asn Leu 80  
65 70 75

Ser Lys Tyr Lys Asp Ser Glu Thr Arg Leu Val Glu Val Leu Glu Gly 95  
85 90

Val Cys Ser Lys Ser Asp Phe Glu Cys His Arg Leu Leu Glu Leu Ser 110  
100 105

Glu Glu Leu Val Glu Ser Trp Trp Phe His Lys Gln Gln Glu Ala Pro 125  
115 120

Asp Leu Phe Gln Trp Leu Cys Ser Asp Ser Leu Lys Leu Cys Cys Pro 140  
130 135

Ala Gly Thr Phe Gly Pro Ser Cys Leu Pro Cys Pro Gly Gly Thr Glu 160  
145 150 155

Arg Pro Cys Gly Gly Tyr Gly Gln Cys Glu Gly Glu Gly Thr Arg Gly 175  
165 170

Gly Ser Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Gly Glu Ala Cys 190  
180 185

Gly Gln Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ala Ser His 205  
195 200

Leu Val Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Ser Gly Pro 220  
210 215

Glu Glu Ser Asn Cys Leu Gln Cys Lys Lys Gly Trp Ala Leu His His 240  
225 230 235

Leu Lys Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gly Ala Asn Cys 255  
245 250

Gly Ala Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg 270  
260 265

Asp Cys Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg 285  
275 280

Cys Lys Lys Cys Ser Pro Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu 300  
290 295

Asp Val Asp Glu Cys Glu Thr Glu Val Cys Pro Gly Glu Asn Lys Gln 320  
305 310 315

Cys Glu Asn Thr Glu Gly Gly Tyr Arg Cys Ile Cys Ala Glu Gly Tyr 335  
325 330

Lys Gln Met Glu Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala 350  
340 345



<210> 113



<211> 1616  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (1461)  
 <223> a, t, c or g

<400> 113  
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 cggggccgcc ctgaccgggg agcagctcct gggcagcctg ctgcggcagc tgcagctcaa 180  
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 ggcccagtac gtggccctgc tgcagcgcag ccacggggac cgctcccgcg gaaagagggt 300  
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 gcgcagcgcc cgggcccggg tgaccgtcga gtggctgcgc gtccgcgacg acggctccaa 540  
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 ctccggagact gactcgctgc ccatgatcgt cagcatcaag gagggaggca ggaccaggcc 1080  
 ccagggtggtc agcctgcccc acatgagggt gcagaagtgc agctgtgcct cggatgggtg 1140  
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 aaagtctcc accaccactc tggacctaa acctgggggt aagtgtgggt tgtgcatccc 1560  
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<210> 114  
 <211> 366  
 <212> PRT  
 <213> Homo sapiens

<400> 114  
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 Ser Pro Gly Ala Ala Leu Thr Gly Glu Gln Leu Leu Gly Ser Leu Leu  
 20 25 30  
 Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met  
 35 40 45

TCCTCCAGGG



Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln Tyr Val Ala Leu  
50 55 60

Leu Gln Arg Ser His Gly Asp Arg Ser Arg Gly Lys Arg Phe Ser Gln  
65 70 75 80

Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr  
85 90 95

His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu  
100 105 110

Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala  
115 120 125

Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg  
130 135 140

Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr  
145 150 155 160

Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys  
165 170 175

Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg  
180 185 190

Pro Arg Gln Pro Leu Leu Leu Gln Val Ser Val Gln Arg Glu His Leu  
195 200 205

Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln  
210 215 220

Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu  
225 230 235 240

Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro  
245 250 255

Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu  
260 265 270

Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro Pro Gly Phe  
275 280 285

Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro Pro Glu Ala Leu  
290 295 300

Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln Cys Ile Ala Ser Glu  
305 310 315 320

Thr Asp Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Gly Arg Thr  
325 330 335



```
<400> 118
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aagtcgcaag tcgagaggaa actgtttgtc ctcttcatat tggcgatcct gttgtgctcc 120
ctggcattgg gcagtgttac agtgcactct tctgaacctg aagtcagaat tcctgagaat 180
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aatcctgtga agttgtcctg tgcctactcg ggcttttctt ctccccgtgt ggagtgggaag 240  
 tttgaccaag gagacaccac cagactcgtt tgctataata acaagatcac agcttcctat 300  
 gaggaccggg tgaccttctt gccaaactggg atcaccttca agtccgtgac acgggaagac 360  
 actgggacat acacttgat ggtctctgag gaaggcggca acagctatgg ggaggtcaag 420  
 gtcaagctca tcgtgcttgt gcctccatcc aagcctacag ttaacatccc ctctctgcc 480  
 accattggga accgggcagt gctgacatgc cctacgaatc ccaaaagcac ccgtgccttc 540  
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 ctctgcctg tctcctgaa tacaagtga ctgacattga ctgtgtctgt ggaaatggg 1620  
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 cagaggctga ggcaggcgga tcacctgagg tcgggagttc gggatcacg tgaccaaac 1800  
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&lt;210&gt; 119

&lt;211&gt; 299

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 119

Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile  
 1 5 10 15

Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His  
 20 25 30

Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu  
 35 40 45

Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe  
 50 55 60

Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr  
 65 70 75 80

Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe  
 85 90 95

090904 0400  
 1020660



<211> 50



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<220>
<223> Description of Artificial Sequence: Synthetic
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## oligonucleotide probe

<400> 125  
actcagcagt ggtaggaaaag

20

<210> 126  
<211> 1210  
<212> DNA  
<213> Homo sapiens

<400> 126  
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gctcaggctc gtgcccaccc accaagttcc agtggccgac cagtggctta tgcgtgcccc 240  
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ggattgagcc atgtacccag aaagggcaat gccaccggcc ccctggcctc ccctgcccc 360  
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ggcgctgcga cggccacca gactgtcccg actccagcga cgagctcggc tgtggaacca 540  
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tgtcctggct ccgagcccag gagcgccctc gccactggg gttactggg gccatgaagg 840  
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ccgtcactca gccctgggcg tagccggaca ggaggagagc agtgatgcgg atgggtaccc 960  
gggcacacca gccctcagag acctgagttc ttctggccac gtggaacctc gaacccgagc 1020  
tcctgcagaa gtggccctgg agattgaggg tcctgggaca ctcctatgg agatccggg 1080  
agctaggatg gggaaacctgc cacagccaga actgaggggc tggccccagg cagctcccag 1140  
ggggtagaac ggccctgtgc ttaagacact ccctgctgcc ccgtctgagg gtggcgatta 1200  
aagttgcttc 1210

<210> 127  
<211> 282  
<212> PRT  
<213> Homo sapiens

<400> 127  
Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala  
1 5 10 15  
Leu Gly Leu Ala Leu Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu  
20 25 30  
Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly  
35 40 45  
Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser  
50 55 60  
Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys  
65 70 75 80

123456789101112131415161718192021222324252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899100



Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln 95  
 85  
 Lys Gly Gln Cys Pro Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly 110  
 100  
 Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Lys Leu Arg Asn Cys Ser 125  
 115  
 Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp 140  
 130  
 Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp 160  
 145  
 Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly 175  
 165  
 Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser 190  
 180  
 Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val 205  
 195  
 Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly 220  
 210  
 Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Val Leu Ser Ala 240  
 225  
 Ser Leu Val Thr Ala Thr Leu Leu Leu Ser Trp Leu Arg Ala Gln 255  
 245  
 Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu 270  
 260  
 Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro 280  
 275

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 128

aagttccagt gccgcaccag tggc

<210> 129



<212> DNA

<211> 21  
<212> DNA  
<213> Artificial Sequence

 $\langle 220 \rangle$ 

```
<212> Sequence
<213> Artificial Sequence
<220> Description of Artificial Sequence: Synthetic
<223> oligonucleotide probe
```

24

<400> 129

<400> 129  
ttggttccac agccgagctc gtcg

<210> 130

$\langle 211 \rangle$  50

<212> DNA

<211> 50  
<212> DNA  
<213> Artificial Sequence

 $\langle 220 \rangle$ 

<212> ~~Sequence~~  
<213> Artificial Sequence  
  
<220> Description of Artificial Sequence: Synthetic  
<223> oligonucleotide probe  
  
gggc aatgcc

50

 $\langle 400 \rangle$  130

```
<223> Description: oligonucleotide primer  
<400> 130  
gaggaggagt gcaggattga gccatgtacc cagaaagggc aatgccacc
```

<210> 131

<210> 152  
<211> 1843

<212> DNA

<212> DNA  
<213> Homo sapiens

 $\langle 220 \rangle$ 

```
<220>
<221> modified_base
      (1837)
```

<221> (1837)

<222> (1837)  
<223> a, t, c or g

<400> 131

```

<221> MODRES: 1
<222> (1837)
<223> a, t, c or g

<400> 131
cccacgcgct cggctctcgct cgctcgcgca gcggcggcag cagaggtcgc gcacagatgc 60
gggttagact ggcggggggga ggaggcgag gaggaagga agtcgcatgc atgagaccga 120
cagactcttg caagctggat gccctctgtg gatgaagat gtatcatgga atgaaccgga 180
gcaatggaga tggatttcta gagcagcagc agcagcagca gcaacctcag tccccccaga 240
gactcttggc cgtgatcctg tggtttcagc tggcgctgtg cttcgccctt gcacagctca 300
cgggcggggt cgatgacctt caagtgtgtg ctgaccgcg cattcccgag aatggcttca 360
ggacccccag cggagggggtt ttctttgaag gctctgtagc ccgatttcac tgccaagacg 420
gattcaagct gaagggcgctt acaagagac tgtgttgaa gcattttaat ggaaccctag 480
gtgggatccc aagtgataat tccatctgtg tgcaagaaga ttgccgtatc cctcaaatcg 540
aagatgctga gattcataac aagacatata gacatggaga gaagctaate atcacttgct 600
atgaaggatt caagatccg taccgcgacc tacacaatat ggtttcatta tgtcgcgatg 660
atggaacgtg gaataatctg gccatctgtc aaggctgcct gagacctcta gcctcttcta 720
atgcgtgctt tcccgattt aaacttgatg ggtctgcgta tcttgagtgc ttacaaaacc 840
ttatctggtc gtccagccca ccccggtgcc cctcctctcc ggtggggact gtgatctcct 900
ctccaatggt gagtcaagga gatttcgtct ttgctctgga agcccaagtc tgtccactac 960
acggaactgt ggtggagttt tactgcgatc gccaccgcg gccttgtag cgctacaacc 1020
acatcacctg ccagtatgga gagtggtttc ctggtacag cctcaccagc gactacaagt 1080
agcaaactg gcccagcacc catgagacc tctgaccac gtggaagatt gtggcggttca 1140

```



```
<210> 132
<211> 490
<212> PRT
<213> Homo sapiens
```

<400> 132

Met Tyr His Gly Met Asn Pro Ser Asn Gly Asp Gly Phe Leu Glu Gln  
1 5 10 15

Gln Gln Gln Gln Gln Gln Pro Gln Ser Pro Gln Arg Leu Leu Ala Val  
20 25 30

Ile Leu Trp Phe Gln Leu Ala Leu Cys Phe Gly Pro Ala Gln Leu Thr  
35 40 45

Gly Gly Phe Asp Asp Leu Gln Val Cys Ala Asp Pro Gly Ile Pro Glu  
50 55 60

Asn Gly Phe Arg Thr Pro Ser Gly Gly Val Phe Phe Glu Gly Ser Val  
65 70 75 80

Ala Arg Phe His Cys Gln Asp Gly Phe Lys Leu Lys Gly Ala Thr Lys  
85 90 95

Arg Leu Cys Leu Lys His Phe Asn Gly Thr Leu Gly Trp Ile Pro Ser  
100 105 110

Asp Asn Ser Ile Cys Val Gln Glu Asp Cys Arg Ile Pro Gln Ile Glu  
115 120 125

Asp Ala Glu Ile His Asn Lys Thr Tyr Arg His Gly Glu Lys Leu Ile  
130 135 140

Ile Thr Cys His Glu Gly Phe Lys Ile Arg Tyr Pro Asp Leu His Asn  
145 150 155 160

Met Val Ser Leu Cys Arg Asp Asp Gly Thr Trp Asn Asn Leu Pro Ile  
165 170 175

Cys Gln Gly Cys Leu Arg Pro Leu Ala Ser Ser Asn Gly Tyr Val Asn



180 185 190  
 Ile Ser Glu Leu Gln Thr Ser Phe Pro Val Gly Thr Val Ile Ser Tyr  
 195 200 205  
 Arg Cys Phe Pro Gly Phe Lys Leu Asp Gly Ser Ala Tyr Leu Glu Cys  
 210 215 220  
 Leu Gln Asn Leu Ile Trp Ser Ser Ser Pro Pro Arg Cys Leu Ala Leu  
 225 230 235 240  
 Glu Ala Gln Val Cys Pro Leu Pro Pro Met Val Ser His Gly Asp Phe  
 245 250 255  
 Val Cys His Pro Arg Pro Cys Glu Arg Tyr Asn His Gly Thr Val Val  
 260 265 270  
 Glu Phe Tyr Cys Asp Pro Gly Tyr Ser Leu Thr Ser Asp Tyr Lys Tyr  
 275 280 285  
 Ile Thr Cys Gln Tyr Gly Glu Trp Phe Pro Ser Tyr Gln Val Tyr Cys  
 290 295 300  
 Ile Lys Ser Glu Gln Thr Trp Pro Ser Thr His Glu Thr Leu Leu Thr  
 305 310 315 320  
 Thr Trp Lys Ile Val Ala Phe Thr Ala Thr Ser Val Leu Leu Val Leu  
 325 330 335  
 Leu Leu Val Ile Leu Ala Arg Met Phe Gln Thr Lys Phe Lys Ala His  
 340 345 350  
 Phe Pro Pro Arg Gly Pro Pro Arg Ser Ser Ser Ser Asp Pro Asp Phe  
 355 360 365  
 Val Val Val Asp Gly Val Pro Val Met Leu Pro Ser Tyr Asp Glu Ala  
 370 375 380  
 Val Ser Gly Gly Leu Ser Ala Leu Gly Pro Gly Tyr Met Ala Ser Val  
 385 390 395 400  
 Gly Gln Gly Cys Pro Leu Pro Val Asp Asp Gln Ser Pro Pro Ala Tyr  
 405 410 415  
 Pro Gly Ser Gly Asp Thr Asp Thr Gly Pro Gly Glu Ser Glu Thr Cys  
 420 425 430  
 Asp Ser Val Ser Gly Ser Ser Glu Leu Leu Gln Ser Leu Tyr Ser Pro  
 435 440 445  
 Pro Arg Cys Gln Glu Ser Thr His Pro Ala Ser Asp Asn Pro Asp Ile  
 450 455 460

180 185 190  
 195 200 205  
 210 215 220  
 225 230 235 240  
 245 250 255  
 260 265 270  
 275 280 285  
 290 295 300  
 305 310 315 320  
 325 330 335  
 340 345 350  
 355 360 365  
 370 375 380  
 385 390 395 400  
 405 410 415  
 420 425 430  
 435 440 445  
 450 455 460



$\langle 211 \rangle$  23

<212> DNA

<211> 25  
<212> DNA  
<213> Artificial Sequence

 $\langle 220 \rangle$ 

<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

23

<400> 133

<400> 133  
atctcctatc gctgctttcc cgg

<210> 134

$\langle 211 \rangle$  23

<212> DNA

```
<211> 23  
<212> DNA  
<213> Artificial Sequence
```

 $\langle 220 \rangle$ 

```
<212> DNA
<213> Artificial Sequence
<220> Description of Artificial Sequence: Synthetic
<223> oligonucleotide probe
```

23

$\langle 400 \rangle$  134

<400> 134  
agccaggatc gcagtaaaac tcc

<210> 135

$\langle 211 \rangle$  50

<212> DNA

```
<211> 50
<212> DNA
<213> Artificial Sequence
```

 $\langle 220 \rangle$ 

```

<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
      atacaa aacctt

```

50

$\langle 400 \rangle$  135

```
<223> Description:
oligonucleotide probe

<400> 135
atttaaactt gatgggtctg cgtatcttga gtgcttacaa aaccttatct
```

<210> 136

$\langle 210 \rangle$  150  
 $\langle 211 \rangle$  1815

<212> DNA

<212> DNA  
<213> Homo sapiens

<400> 136

```

<211> 1815
<212> DNA
<213> Homo sapiens

<400> 136
cccacgcgctc cgctccgcgc cctccccccc gcctcccgctg cgggtccgctcg gtggcctaga 60
gatgctgctg ccgcgggttc agttgtcgcg cacgcctctg cccgccagcc cgctccaccg 120
ccgtagcgcc cgagtgtcgg gggggcgacc cgagtcgggc catgaggccg ggaaccgcgc 180
tacaggccgt gctgctggcc gtgctgctgg tggggctgcg ggccgcgacg ggtcgctgc 240
tgagtgcctc ggatttggac ctcacaggag ggcagccagt ctgccgggga gggacacaga 300

```



ggcccttggtta taaagtcatt tacttccatg atacttctcg aagactgaac tttgaggaag 360  
 ccaaagaagc ctgcaggagg gatggaggcc agctagtcag catcgagtct gaagatgaac 420  
 agaaactgat agaaaagttc attgaaaacc tcttgccatc tgatggtgac ttctggattg 480  
 ggctcaggag gcgtgaggag aaacaaagca atagcacagc ctgccaggac ctttatgctt 540  
 ggactgatgg cagcatatca caatttagga actggtatgt ggatgagccg tcctgcgga 600  
 gcgaggtctg cgtgggtcatg taccatcagc catcggcacc cgctggcatc ggaggcccct 660  
 acatgttcca gtggaatgat gaccgggtgca acatgaagaa caatttcatt tgcaaatatt 720  
 ctgatgagaa accagcagtt ccttctagag aagctgaagg tgaggaaaca gagctgacaa 780  
 cacctgtact tccagaagaa acacaggaag aagatgcca aaaaacattt aaagaaagta 840  
 gagaagctgc cttgaatctg gcctacatcc taatccccag cattcccctt ctcctcctcc 900  
 ttgtggtcac cacagttgta tggtgggttt ggatctgtag aaaaagaaaa cgggagcagc 960  
 cagaccctag cacaagaag caacacacca tctggccctc tcctcaccag ggaaacagcc 1020  
 cggacctaga ggtctacaat gtcataagaa aacaaagcga agctgactta gctgagaccc 1080  
 ggccagacct gaagaatatt tcattccgag tgtgttcggg agaagccact cccgatgaca 1140  
 tgtcttgtga ctatgacaac atggctgtga acccatcaga aagtgggttt gtgactctgg 1200  
 tgagcgtgga gagtggattt gtgaccaatg acatttatga gttctcccca gaccaaattg 1260  
 ggaggagtaa ggagtctgga tgggtggaaa atgaaatata tggttattag gacatataaa 1320  
 aaactgaaac tgacaacaat ggaaaagaaa tgataagcaa aatcctctta tttctataa 1380  
 ggaaaataca cagaaggtct atgaacaagc ttagatcagg tcctgtggat gagcatgtgg 1440  
 tccccacgac ctctgttggtg acccccacgt tttggctgta tcctttatcc cagccagtca 1500  
 tccagctcga ccttatgaga aggtaccttg cccaggtctg gcacatagta gagtctcaat 1560  
 aaatgtcact tggttggttg tatctaactt ttaagggaca gagctttacc tggcagtgat 1620  
 aaagatgggc tgtggagctt ggaaaaccac ctctgttttc cttgctctat acagcagcac 1680  
 atattatcat acagacagaa aatccagaat cttttcaaag cccacatatg gtagcacagg 1740  
 ttggcctgtg catcggaat tctcatatct gtttttttca aagaataaaa tcaaataaag 1800  
 agcaggaaaa aaaaa 1815

<210> 137  
 <211> 382  
 <212> PRT  
 <213> Homo sapiens

<400> 137  
 Met Arg Pro Gly Thr Ala Leu Gln Ala Val Leu Leu Ala Val Leu Leu  
 1 5 10 15  
 Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu  
 20 25 30  
 Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro  
 35 40 45  
 Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe  
 50 55 60  
 Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser  
 65 70 75 80  
 Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn  
 85 90 95  
 Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Arg Glu  
 100 105 110

0900204-071001



Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr  
 115 120 125  
 Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser  
 130 135 140  
 Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro  
 145 150 155 160  
 Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys  
 165 170 175  
 Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala  
 180 185 190  
 Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro  
 195 200 205  
 Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys  
 210 215 220  
 Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser  
 225 230 235 240  
 Ile Pro Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val  
 245 250 255  
 Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys  
 260 265 270  
 Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp  
 275 280 285  
 Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala Asp Leu Ala  
 290 295 300  
 Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly  
 305 310 315 320  
 Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val  
 325 330 335  
 Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly  
 340 345 350  
 Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln Met Gly Arg  
 355 360 365  
 Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly Tyr  
 370 375 380  
 <210> 138



<211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 138  
 gttcattgaa aacctcttgc catctgatgg tgacttctgg attgggctca

50

<210> 139  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

24

<400> 139  
 aagccaaaga agcctgcagg aggg

<210> 140  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

24

<400> 140  
 cagtccaagc ataaagggtcc tggc

<210> 141  
 <211> 1514  
 <212> DNA  
 <213> Homo sapiens

<400> 141  
 ggggtctccc tcagggccgg gaggcacagc ggctccctgct tgctgaaggg ctggatgtac 60  
 gcatccgcag gttcccgcgg acttgggggc gcccgtgag ccccgccgcc cgcagaagac 120  
 ttgtgtttgc ctctgcagc ctcaaccggg agggcagcga gggcctacca ccatgatcac 180  
 tgggtgtgtc agcatgcgct tgtggacccc agtgggcgtc ctgacctcgc tggcgactctg 240  
 cctgcaccag cggcgggtgg ccctggccga gctgcaggag gccgatggcc agtgtccggt 300  
 cgaccgcagc ctgctgaagt tgaaaatggt gcaggctcgtg ttctgacacg gggctcggag 360  
 tcctctcaag ccgctcccgc tggaggagca ggtagagtgg aacccccagc tattagaggt 420  
 cccaccccaa actcagtttg attacacagt caccaatcta gctgggtggtc cgaaaccata 480  
 ttctccttac gactctcaat accatgagac caccctgaag gggggcatgt ttgctgggca 540  
 gctgaccaag gtgggcatgc agcaaatgtt tgccttggga gagagactga ggaagaacta 600  
 tgtggaagac attccctttc ttccaccaac cttcaaccca caggaggtct ttattcggtc 660  
 cactaacatt ttccggaatc tggagtcac cgttggtttg ctggctgggc tttccagtg 720







```
<210> 143
<211> 24
<212> DNA
<213> Artificial Sequence
```



24

```
<210> 144
<211> 24
<212> DNA
<213> Artificial Sequence
```

24

```
<210> 145
<211> 24
<212> DNA
<213> Artificial Sequence
```

24

```
<210> 146
<211> 45
<212> DNA
<213> Artificial Sequence
```

45

```
<210> 147
<211> 1686
<212> DNA
<213> Homo sapiens
```

```

<400> 147
ctcctcttaa catacttgca gctaaaacta aatattgctg cttggggacc tccttctagc 60
cttaaatttc agctcatcac cttcacctgc cttggctcatg gctctgctat tctccttgat 120
ccttgccatt tgcaccagac ctggattcct agcgtctcca tctggagtgc ggctggtggg 180

```



```
<210> 148
<211> 347
<212> PRT
<213> Homo sapiens
```

213> NCBI  
<400> 148  
Met Ala Leu Leu Phe Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro Gly  
1 5 10 15  
Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg  
20 25 30  
Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val  
35 40 45  
Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu  
50 55 60  
Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu  
65 70 75 80  
Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys  
85 90 95  
Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr  
100 105 110



<220>  
<223> Description of Artificial Sequence: Synthetic



24

```
<210> 150
<211> 24
<212> DNA
<213> Artificial Sequence
```

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 150  
ggctcataca aaataccact aggg

```
<210> 151
<211> 50
<212> DNA
<213> Artificial Sequence
```

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 151  
gggcctccac cgctgtgaag ggcggtgga ggtggaacag aaaggccagt

```
<210> 152
<211> 1427
<212> DNA
<213> Homo sapiens
```

<400> 152									
actgcactcg	gttctatcga	ttgaattccc	cggggatcct	ctagagatcc	ctcgacctcg	60			
accacacgcg	ccgcggacgc	gtgggcggac	gcgtgggccc	gctaccagga	agagtctgcc	120			
gaaggtgaag	gccatggact	tcatcacctc	cacagccatc	ctgccctcgc	tgttcggctg	180			
cctgggcgtc	ttcggcctct	tccggctgct	gcagtgggtg	cgcgggaagg	cctacctgcg	240			
gaatgctgtg	gtgggtgatca	caggcgccac	ctcagggctg	ggcaagaat	gtgcaaaagt	300			
cttctatgct	gcgggtgcta	aactgggtgt	ctgtggccgg	aatggtgggg	ccctagaaga	360			
gctcatcaga	gaacttaccg	cttctcatgc	caccaagggtg	cagacacaca	agccttactt	420			
ggtgaccttc	gacctcacag	actctggggc	catagttgca	gcagcagctg	agatcctgca	480			
gtgctttggc	tatgtcgaca	tacttgtcaa	caatgctggg	atcagctacc	gtggtaccat	540			
catggacacc	acagtggatg	tggacaagag	ggtcatggag	acaaactact	ttggcccagt	600			
tgctctaacg	aaagcactcc	tggcctccat	gatcaagagg	aggcaaggcc	acattgtcgc	660			
catcagcagc	atccagggca	agatgagcat	tctttttcga	tcagcatatg	cagcctccaa	720			
gcacgcaacc	caggctttct	ttgactgtct	gcgtgccgag	atggaacagt	atgaaattga	780			
ggtgaccgtc	atcagccccg	gctacatcca	caccaacctc	tctgtaaatg	ccatcaccgc	840			
ggatggatct	aggtatggag	ttatggacac	caccacagcc	cagggccgaa	gcctgtgga	900			
ggtggcccag	gatgttcttg	ctgctgtggg	gaagaagaag	aaagatgtga	tctctggctga	960			
cttactgctc	tccttggtcg	tttatcttcg	aactctggct	cctgggctct	tcttcagcct	1020			
catggcctcc	agggccagaa	aagagcggaa	atccaagaac	tcttagtact	ctgaccagcg	1080			



$\langle 211 \rangle$  310

<212> PRT

<212> PRT  
<213> Homo sapiens

<400> 153

Met Asp Phe Ile Thr Ser  
1 5  
Phe Arg Leu Leu Gln Trp Val Arg Gly  
30

1  
Leu Gly Val Phe Gly Leu Phe Arg Leu 25  
20 Val Ile Thr Gly Ala Thr Ser Gly 45

Ala Tyr Leu Arg Asn Ala Val Val Val Val  
35 40 60

Val Phe Tyr Ala Ala Gly Ala Lys Leu

Leu Gly Lys Glu Cys Ala Lys Val Phe 60  
50 55  
Gly Ala Leu Glu Glu Leu Ile Arg Glu 80  
75

Val Leu Cys Gly Arg Asn Gly Gly Ala 75  
65 70 95  
Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu  
90

65  
Leu Thr Ala Ser His Ala Thr Lys Val 90  
85  
Gly Ala Ile Val Ala Ala Ala Ala  
110

Val Thr Phe Asp Leu Thr Asp Ser Gly Asn  
100  
Val Asp Ile Leu Val Asn Asn Ala  
125

Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp  
115 120 125  
130 Met Asp Thr Thr Val Asp Val Asp  
140

Gly Ile Ser Tyr Arg Gly Thr Ile Met Lys  
130 135 140  
Lan Tyr Phe Gly Pro Val Ala Leu Thr Lys  
155 160

Lys Arg Val Met Glu Thr Asn Tyr 150  
145 Met Ile Lys Arg Arg Gln Gly His Ile Val Ala 175

145  
Ala Leu Leu Pro Ser Met Ile Lys Arg 170  
165  
Ser Ile Pro Phe Arg Ser Ala Tyr  
190

Ile Ser Ser Ile Gln Gly Lys Met Ser 185  
180 Ala Phe Phe Asp Cys Leu Arg Ala 205

Ala Ala Ser Lys His Ala Thr Gln Ala  
195 200  
Gly Val Thr Val Ile Ser Pro Gly Tyr

Ala Ala 195  
Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val



210  
 Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg  
 225 230 235 240  
 Tyr Gly Val Met Asp Thr Thr Thr Ala Gln Gly Arg Ser Pro Val Glu  
 245 250 255  
 Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Lys Asp Val  
 260 265 270  
 Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu  
 275 280 285  
 Ala Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg Ala Arg Lys Glu  
 290 295 300  
 Arg Lys Ser Lys Asn Ser  
 305 310

<210> 154  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

24

<400> 154  
 ggtgctaaac tgggtgctctg tggc

<210> 155  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

20

<400> 155  
 cagggaaga tgagcattcc

<210> 156  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

0900204 0700660



<400> 156  
tcatactggt ccatctcggc acgc

<210> 157  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

50

<400> 157  
aatggtgggg ccctagaaga gctcatcaga gaactcaccg cttctcatgc

<210> 158  
<211> 1771  
<212> DNA  
<213> Homo sapiens

<400> 158  
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cctcctgctt ctcccgttac tgatcgctcg ctccctagag tccttcgtga agctttttat 180  
tcctaagagg agaaaatcag tcaccggcga aatcgctgctg attacaggag ctgggcatgg 240  
aattgggaga ctgactgcct atgaatttgc taaacttaaa agcaagctgg ttctctggga 300  
tataaataag catggactgg aggaacacgc tgccaaatgc aagggactgg gtgccaaggt 360  
tcataccttt gtggtagact gcagcaaccg agaagatatt tacagctctg caaagaaggt 420  
gaaggcagaa attggagatg ttagtatttt agtaataat gctggtgtag tctatacatc 480  
agatttgttt gctacacaag atcctcagat tgaaaagact tttgaagtta atgtacttgc 540  
acatttctgg actacaaagg catttcttc tgcaatgacg aagaataacc atggccatat 600  
tgtcactgtg gcttcggcag ctggacatgt ctcggtccc ttcttactgg cttactgttc 660  
aagcaagttt gctgctgttg gatttcataa aactttgaca gatgaactgg ctgccttaca 720  
aataactgga gtcaaaaaca catgtctgtg tcctaatttc gtaaacactg gcttcatcaa 780  
aaatccaagt acaagtttgg gaccactctt ggaacctgag gaagtggtaa acaggctgat 840  
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<210> 159

158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999



<211> 300  
 <212> PRT  
 <213> Homo sapiens

<400> 159  
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 Cys Ser Leu Glu Ser Phe Val Lys Leu Phe Ile Pro Lys Arg Arg Lys  
 20 25 30  
 Ser Val Thr Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His Gly Ile  
 35 40 45  
 Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Lys Ser Lys Leu Val  
 50 55 60  
 Leu Trp Asp Ile Asn Lys His Gly Leu Glu Glu Thr Ala Ala Lys Cys  
 65 70 75 80  
 Lys Gly Leu Gly Ala Lys Val His Thr Phe Val Val Asp Cys Ser Asn  
 85 90 95  
 Arg Glu Asp Ile Tyr Ser Ser Ala Lys Lys Val Lys Ala Glu Ile Gly  
 100 105 110  
 Asp Val Ser Ile Leu Val Asn Asn Ala Gly Val Val Tyr Thr Ser Asp  
 115 120 125  
 Leu Phe Ala Thr Gln Asp Pro Gln Ile Glu Lys Thr Phe Glu Val Asn  
 130 135 140  
 Val Leu Ala His Phe Trp Thr Thr Lys Ala Phe Leu Pro Ala Met Thr  
 145 150 155 160  
 Lys Asn Asn His Gly His Ile Val Thr Val Ala Ser Ala Ala Gly His  
 165 170 175  
 Val Ser Val Pro Phe Leu Leu Ala Tyr Cys Ser Ser Lys Phe Ala Ala  
 180 185 190  
 Val Gly Phe His Lys Thr Leu Thr Asp Glu Leu Ala Ala Leu Gln Ile  
 195 200 205  
 Thr Gly Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val Asn Thr Gly  
 210 215 220  
 Phe Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu Glu Pro Glu  
 225 230 235 240  
 Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu Gln Lys Met  
 245 250 255

000004 01000000



Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu Arg Ile  
260 265 270

Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile Ser Val Lys  
275 280 285

Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln  
290 295 300

<210> 160

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

23

<400> 160

ggtgaaggca gaaattggag atg

<210> 161

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

24

<400> 161

atcccatgca tcagcctggt tacc

<210> 162

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

48

<400> 162

gctggtgtag tctatacatc agatttggtt gctacacaag atcctcag

<210> 163

<211> 2076

<212> DNA

<213> Homo sapiens

<400> 163

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<210> 164
<211> 476
<212> PRT
<213> Homo sapiens
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20 25 30  
Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr  
35 40 45  
Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly  
50 55 60  
Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val



65 70 75 80

Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe Trp Phe Phe Pro Ala Gln  
85 90 95

Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly Gly Pro  
100 105 110

Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro Tyr Val  
115 120 125

Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp Thr Thr  
130 135 140

Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly Phe Ser  
145 150 155 160

Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp Val Ala  
165 170 175

Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro Glu  
180 185 190

Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys  
195 200 205

Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg  
210 215 220

Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly Tyr Ser  
225 230 235 240

Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr Gln Ile  
245 250 255

Gly Leu Leu Asp Glu Lys Gln Lys Lys Tyr Phe Gln Lys Gln Cys His  
260 265 270

Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala Phe Glu  
275 280 285

Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro Ser Tyr  
290 295 300

Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu Arg Cys  
305 310 315 320

Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser Leu Pro  
325 330 335

Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn Asp Gly  
340 345 350



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<210> 167
<211> 24
<212> DNA
<213> Artificial Sequence
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24



24

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<210> 168
<211> 50
<212> DNA
<213> Artificial Sequence
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50

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<210> 169
<211> 2477
<212> DNA
<213> Homo sapiens
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Accession	Gene	Species	Length (bp)
<213>	Homo sapiens		
<400>	169		
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tcttgctgga	gaagaaagg	ctgagggcag	agcagggcac
tccctgcctc	tctgtggata	acagagcatg	agaaagtga
gatggaagtc	taaaatagga	aggaattttg	tgtgcaatat
cctggagagc	ctggggggag	gcctgcctaa	caagctttca
ctgggctggg	ataagacgtg	ccggttaggat	aggggaagact
attgactggc	tgggtgaact	tcaacagcct	tttaacctct
cttaaggggc	cagaaataga	gatgctttgt	aaaataaaat
tatagcataa	aggctagaga	ccaaaataga	taacaggatt
gagaaagtat	gttaaaaata	gaaaaaccaa	aatgcagaag
accaggatgg	ggaccctggg	tccaggccagc	ctctttgctc
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tgggtgctgc	tggccccccc	agcagccggc	atgcctcagt
aatcgtgact	ggaccttcaa	ccacttgacc	gtccaccaag
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```
<210> 170
<211> 552
<212> PRT
<213> Homo sapiens
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Met Gly Thr Leu Cys 15  
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Gln Pro Gly Lys Val 40  
 35  
 Thr Ala Ala Pro Leu Ser Met Glu Gln Arg Gln Pro Trp Pro Arg Ala 60  
 50 55  
 Leu Ser Val Val Trp Val

Leu Glu Val Asp Ser 70  
65  
Leu Leu Ala Pro Pro Ala Ala Gly Met Pro Gln Phe Ser Thr Phe His 95  
85  
His Gln Gly

Ser Glu Asn Arg Asp 105  
100  
Thr Gly Ala Val Tyr Val Gly Ala Ile Asn Arg Val Tyr Lys Leu Thr 125  
115  
Gly Pro Glu Glu Asp

Gly Asn Leu Thr Ile 135  
130  
Asn Lys Ser Arg Tyr Pro Pro Leu Ile Val Gln Pro Cys Ser Glu Val 160  
145 150 155  
Leu Leu Ile Ile Asp Tyr Ser

Asn Lys Ser Arg 145 150  
Leu Thr Leu Thr Asn Asn Val Asn Lys Leu Leu Ile Ile Asp Tyr Ser 175  
165 170



Glu Asn Arg Leu Leu Ala Cys Gly Ser Leu Tyr Gln Gly Val Cys Lys  
180 185 190

Leu Leu Arg Leu Asp Asp Leu Phe Ile Leu Val Glu Pro Ser His Lys  
195 200 205

Lys Glu His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly  
210 215 220

Val Ile Val Arg Ser Glu Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr  
225 230 235 240

Ala Val Asp Gly Lys Gln Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys  
245 250 255

Leu Pro Arg Asp Pro Glu Ser Ser Ala Met Leu Asp Tyr Glu Leu His  
260 265 270

Ser Asp Phe Val Ser Ser Leu Ile Lys Ile Pro Ser Asp Thr Leu Ala  
275 280 285

Leu Val Ser His Phe Asp Ile Phe Tyr Ile Tyr Gly Phe Ala Ser Gly  
290 295 300

Gly Phe Val Tyr Phe Leu Thr Val Gln Pro Glu Thr Pro Glu Gly Val  
305 310 315 320

Ala Ile Asn Ser Ala Gly Asp Leu Phe Tyr Thr Ser Arg Ile Val Arg  
325 330 335

Leu Cys Lys Asp Asp Pro Lys Phe His Ser Tyr Val Ser Leu Pro Phe  
340 345 350

Gly Cys Thr Arg Ala Gly Val Glu Tyr Arg Leu Leu Gln Ala Ala Tyr  
355 360 365

Leu Ala Lys Pro Gly Asp Ser Leu Ala Gln Ala Phe Asn Ile Thr Ser  
370 375 380

Gln Asp Asp Val Leu Phe Ala Ile Phe Ser Lys Gly Gln Lys Gln Tyr  
385 390 395 400

His His Pro Pro Asp Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala  
405 410 415

Ile Asn Leu Gln Ile Lys Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu  
420 425 430

Gly Asn Leu Glu Leu Asn Trp Leu Leu Gly Lys Asp Val Gln Cys Thr  
435 440 445

Lys Ala Pro Val Pro Ile Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn



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<210> 171
<211> 20
<212> DNA
<213> Artificial Sequence
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20

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<210> 172
<211> 24
<212> DNA
<213> Artificial Sequence
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24

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<210> 173
<211> 43
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe



42

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<210> 174
<211> 3106
<212> DNA
<213> Homo sapiens
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<223> a, t, c or g
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gccctgcatt	acagttcacg	gaaaccccc	acctgggcag	gaaccagtac	attaagtgag	1980	
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<210> 175
<211> 636
<212> PRT
<213> Homo sapiens
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<221> MOD_RES  
<222> (539)  
<223> Any amino acid
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			20					25					30				
Ser	Thr	Leu	Val	Pro	Leu	Arg	Leu	Arg	His	Arg	Gln	Leu	Gly	Leu	Gln		
		35					40					45					
Ala	Lys	Gly	Trp	Asn	Phe	Met	Leu	Glu	Asp	Ser	Thr	Phe	Trp	Ile	Phe		
	50					55						60					
Gly	Gly	Ser	Ile	His	Tyr	Phe	Arg	Val	Pro	Arg	Glu	Tyr	Trp	Arg	Asp		
65					70					75					80		
Arg	Leu	Leu	Lys	Met	Lys	Ala	Cys	Gly	Leu	Asn	Thr	Leu	Thr	Thr	Tyr		
				85					90					95			
Val	Pro	Trp	Asn	Leu	His	Glu	Pro	Glu	Arg	Gly	Lys	Phe	Asp	Phe	Ser		
			100					105					110				
Gly	Asn	Leu	Asp	Leu	Glu	Ala	Phe	Val	Leu	Met	Ala	Ala	Glu	Ile	Gly		
		115					120					125					
Leu	Trp	Val	Ile	Leu	Arg	Pro	Gly	Pro	Tyr	Ile	Cys	Ser	Glu	Met	Asp		
	130					135					140						



Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met Arg Leu  
 145 150 155 160  
 Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr Phe Asp  
 165 170 175  
 His Leu Met Ser Arg Val Val Pro Leu Gln Tyr Lys Arg Gly Gly Pro  
 180 185 190  
 Ile Ile Ala Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn Lys Asp  
 195 200 205  
 Pro Ala Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg Gly Ile  
 210 215 220  
 Val Glu Leu Leu Leu Thr Ser Asp Asn Lys Asp Gly Leu Ser Lys Gly  
 225 230 235 240  
 Ile Val Gln Gly Val Leu Ala Thr Ile Asn Leu Gln Ser Thr His Glu  
 245 250 255  
 Leu Gln Leu Leu Thr Thr Phe Leu Phe Asn Val Gln Gly Thr Gln Pro  
 260 265 270  
 Lys Met Val Met Glu Tyr Trp Thr Gly Trp Phe Asp Ser Trp Gly Gly  
 275 280 285  
 Pro His Asn Ile Leu Asp Ser Ser Glu Val Leu Lys Thr Val Ser Ala  
 290 295 300  
 Ile Val Asp Ala Gly Ser Ser Ile Asn Leu Tyr Met Phe His Gly Gly  
 305 310 315 320  
 Thr Asn Phe Gly Phe Met Asn Gly Ala Met His Phe His Asp Tyr Lys  
 325 330 335  
 Ser Asp Val Thr Ser Tyr Asp Tyr Asp Ala Val Leu Thr Glu Ala Gly  
 340 345 350  
 Asp Tyr Thr Ala Lys Tyr Met Lys Leu Arg Asp Phe Phe Gly Ser Ile  
 355 360 365  
 Ser Gly Ile Pro Leu Pro Pro Pro Pro Asp Leu Leu Pro Lys Met Pro  
 370 375 380  
 Tyr Glu Pro Leu Thr Pro Val Leu Tyr Leu Ser Leu Trp Asp Ala Leu  
 385 390 395 400  
 Lys Tyr Leu Gly Glu Pro Ile Lys Ser Glu Lys Pro Ile Asn Met Glu  
 405 410 415  
 Asn Leu Pro Val Asn Gly Gly Asn Gly Gln Ser Phe Gly Tyr Ile Leu  
 420 425 430

145 150 155 160  
 165 170 175  
 180 185 190  
 195 200 205  
 210 215 220  
 225 230 235 240  
 245 250 255  
 260 265 270  
 275 280 285  
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<210> 176
<211> 2505
<212> DNA
<213> Homo sapiens
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aaggggagca	aagccgggct	cggccccagg	cccccaggac	ctccatctcc	caatgttggg	180	
ggaatccgac	acgtgacggg	ctgtccgcgc	tctcagacta	gaggagcgct	gtaaacgcca	240	
tggctcccaa	gaagetgtcc	tgccttcggt	ccctgctgct	gccgctcagc	ctgacgctac	300	
tgctgcccc	ggcagacact	cggtcgttcg	tagtggaatg	gggtcatgac	cggtttctcc	360	
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<210> 177
<211> 654
<212> PRT
<213> Homo sapiens
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      20             25             30

Asp Arg Gly His Asp Arg Phe Leu Leu Asp Gly Ala Pro Phe Arg Tyr
      35             40             45

Val Ser Gly Ser Leu His Tyr Phe Arg Val Pro Arg Val Leu Trp Ala
      50             55             60

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Asp 65	Arg	Leu	Leu	Lys	Met 70	Arg	Trp	Ser	Gly	Leu 75	Asn	Ala	Ile	Gln	Phe 80
Tyr	Val	Pro	Trp	Asn 85	Tyr	His	Glu	Pro	Gln 90	Pro	Gly	Val	Tyr	Asn 95	Phe
Asn	Gly	Ser	Arg 100	Asp	Leu	Ile	Ala	Phe 105	Leu	Asn	Glu	Ala	Ala	Leu	Ala
Asn	Leu	Leu	Val 115	Ile	Leu	Arg	Pro 120	Gly	Pro	Tyr	Ile	Cys 125	Ala	Glu	Trp
Glu 130	Met	Gly	Gly	Leu	Pro	Ser 135	Trp	Leu	Leu	Arg	Lys 140	Pro	Glu	Ile	His
Leu 145	Arg	Thr	Ser	Asp 150	Pro	Asp	Phe	Leu	Ala	Ala 155	Val	Asp	Ser	Trp	Phe 160
Lys	Val	Leu	Leu	Pro 165	Lys	Ile	Tyr	Pro	Trp 170	Leu	Tyr	His	Asn	Gly 175	Gly
Asn	Ile	Ile	Ser 180	Ile	Gln	Val	Glu	Asn 185	Glu	Tyr	Gly	Ser	Tyr	Arg	Ala
Cys	Asp	Phe	Ser 195	Tyr	Met	Arg	His 200	Leu	Ala	Gly	Leu	Phe 205	Arg	Ala	Leu
Leu 210	Gly	Glu	Lys	Ile	Leu	Leu 215	Phe	Thr	Thr	Asp	Gly 220	Pro	Glu	Gly	Leu
Lys 225	Cys	Gly	Ser	Leu	Arg 230	Gly	Leu	Tyr	Thr	Thr 235	Val	Asp	Phe	Gly	Pro 240
Ala	Asp	Asn	Met 245	Thr	Lys	Ile	Phe	Thr	Leu 250	Leu	Arg	Lys	Tyr	Glu 255	Pro
His	Gly	Pro	Leu 260	Val	Asn	Ser	Glu	Tyr 265	Tyr	Thr	Gly	Trp	Leu	Asp 270	Tyr
Trp	Gly	Gln	Asn 275	His	Ser	Thr	Arg 280	Ser	Val	Ser	Ala	Val 285	Thr	Lys	Gly
Leu 290	Glu	Asn	Met	Leu	Lys 295	Leu	Gly	Ala	Ser	Val	Asn 300	Met	Tyr	Met	Phe
His 305	Gly	Gly	Thr	Asn 310	Phe	Gly	Tyr	Trp	Asn	Gly 315	Ala	Asp	Lys	Lys	Gly 320
Arg	Phe	Leu	Pro 325	Ile	Thr	Thr	Ser	Tyr	Asp 330	Tyr	Asp	Ala	Pro	Ile 335	Ser
Glu	Ala	Gly	Asp	Pro	Thr	Pro	Lys	Leu	Phe	Ala	Leu	Arg	Asp	Val	Ile



340							345					350				
Ser	Lys	Phe	Gln	Glu	Val	Pro	Leu	Gly	Pro	Leu	Pro	Pro	Pro	Ser	Pro	
		355					360					365				
Lys	Met	Met	Leu	Gly	Pro	Val	Thr	Leu	His	Leu	Val	Gly	His	Leu	Leu	
	370					375					380					
Ala	Phe	Leu	Asp	Leu	Leu	Cys	Pro	Arg	Gly	Pro	Ile	His	Ser	Ile	Leu	
385					390					395					400	
Pro	Met	Thr	Phe	Glu	Ala	Val	Lys	Gln	Asp	His	Gly	Phe	Met	Leu	Tyr	
				405					410					415		
Arg	Thr	Tyr	Met	Thr	His	Thr	Ile	Phe	Glu	Pro	Thr	Pro	Phe	Trp	Val	
			420					425					430			
Pro	Asn	Asn	Gly	Val	His	Asp	Arg	Ala	Tyr	Val	Met	Val	Asp	Gly	Val	
		435					440					445				
Phe	Gln	Gly	Val	Val	Glu	Arg	Asn	Met	Arg	Asp	Lys	Leu	Phe	Leu	Thr	
	450					455					460					
Gly	Lys	Leu	Gly	Ser	Lys	Leu	Asp	Ile	Leu	Val	Glu	Asn	Met	Gly	Arg	
465					470					475					480	
Leu	Ser	Phe	Gly	Ser	Asn	Ser	Ser	Asp	Phe	Lys	Gly	Leu	Leu	Lys	Pro	
				485					490					495		
Pro	Ile	Leu	Gly	Gln	Thr	Ile	Leu	Thr	Gln	Trp	Met	Met	Phe	Pro	Leu	
			500					505					510			
Lys	Ile	Asp	Asn	Leu	Val	Lys	Trp	Trp	Phe	Pro	Leu	Gln	Leu	Pro	Lys	
		515					520					525				
Trp	Pro	Tyr	Pro	Gln	Ala	Pro	Ser	Gly	Pro	Thr	Phe	Tyr	Ser	Lys	Thr	
	530					535					540					
Phe	Pro	Ile	Leu	Gly	Ser	Val	Gly	Asp	Thr	Phe	Leu	Tyr	Leu	Pro	Gly	
545					550					555					560	
Trp	Thr	Lys	Gly	Gln	Val	Trp	Ile	Asn	Gly	Phe	Asn	Leu	Gly	Arg	Tyr	
				565					570					575		
Trp	Thr	Lys	Gln	Gly	Pro	Gln	Gln	Thr	Leu	Tyr	Val	Pro	Arg	Phe	Leu	
			580					585					590			
Leu	Phe	Pro	Arg	Gly	Ala	Leu	Asn	Lys	Ile	Thr	Leu	Leu	Glu	Leu	Glu	
		595					600					605				
Asp	Val	Pro	Leu	Gln	Pro	Gln	Val	Gln	Phe	Leu	Asp	Lys	Pro	Ile	Leu	
	610					615					620					



Asn Ser Thr Ser Thr Leu His Arg Thr His Ile Asn Ser Leu Ser Ala  
 625 630 635 640

Asp Thr Leu Ser Ala Ser Glu Pro Met Glu Leu Ser Gly His  
 645 650

<210> 178

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 178

tggctactcc aagaccctgg catg

24

<210> 179

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 179

tggacaaatc cccttgctca gccc

24

<210> 180

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 180

gggcttcacc gaagcagtgg acctttattt tgaccacctg atgtccaggg

50

<210> 181

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 181

ccagctatga ctatgatgca cc

22

108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000



<400> 184						
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gtgtttatgg	ctttatctgc	ctctacactc	tcttctgggt	attcaggata	cctttgaagg	180
aatattcttt	cgaaaaagtc	agagaagaga	gcagttttag	tgacattcca	gatgtcaaaa	240
acgattttgc	gttccttctt	cacatggtag	accagtatga	ccagctatat	tccaagcgtt	300
ttggtgtggt	cttgtcagaa	gttagtgaaa	ataaacttag	ggaaatttag	ttgaaccatg	360
agtggacatt	tgaaaaactc	aggcagcaca	tttcacgcaa	cgcccaggac	aagcaggagt	420
tgcattctgtt	catgctgtcg	ggggcgcccg	atgctgtctt	tgacctcaca	gacctggatg	480
tgctaaagct	tgaactaatt	ccgaagctca	aaattcctgc	taagatttct	caaatgacta	540
acctccaaga	gctccacctc	tgccactgcc	ctgcaaaagt	tgaacagact	gcttttagct	600
ttcttcgcga	tcacttgaga	tgctttcacg	tgaagttcac	tgatgtggct	gaaattcctg	660
cctgggtgta	tttgctcaaa	aaccttcgag	agttgtactt	aataggcaat	ttgaactctg	720
aaaacaataa	gatgatagga	cttgaatctc	tccgagagtt	gcggcacctt	aagattctcc	780
acgtgaagag	caatttgacc	aaagttccct	ccaacattac	agatgtggct	ccacatctta	840
caaagttagt	cattcataat	gacggcacta	aactcttggt	actgaacagc	cttaagaaaa	900
tgatgaatgt	cgctgagctg	gaactccaga	actgtgagct	agagagaatc	ccacatgcta	960
ttttcagcct	ctctaattta	caggaactgg	atttaaagtc	caataacatt	cgcacaattg	1020
aggaaatcat	cagtttccag	cattttaaacc	gactgacttg	ttttaaatta	tggcataaca	1080
aaattgttac	tattcctccc	tctattatccc	atgtcaaaaa	cttgagagtc	ctttatttct	1140
ctaacaacaa	gctcgaatac	ttaccagtgg	cagtattttag	tttcagaaaa	cttcagatgct	1200
tagatgtgag	ctacaacaac	atttcaatga	ttccaataga	aataggattg	cttcagaacc	1260
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<210> 185
<211> 501
<212> PRT
<213> Homo sapiens
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			20					25					30			
Ile	Pro	Leu	Lys	Glu	Tyr	Ser	Phe	Glu	Lys	Val	Arg	Glu	Glu	Ser	Ser	
		35					40					45				
Phe	Ser	Asp	Ile	Pro	Asp	Val	Lys	Asn	Asp	Phe	Ala	Phe	Leu	Leu	His	
	50					55					60					
Met	Val	Asp	Gln	Tyr	Asp	Gln	Leu	Tyr	Ser	Lys	Arg	Phe	Gly	Val	Phe	
65					70					75					80	
Leu	Ser	Glu	Val	Ser	Glu	Asn	Lys	Leu	Arg	Glu	Ile	Ser	Leu	Asn	His	
				85					90					95		
Glu	Trp	Thr	Phe	Glu	Lys	Leu	Arg	Gln	His	Ile	Ser	Arg	Asn	Ala	Gln	
			100					105					110			
Asp	Lys	Gln	Glu	Leu	His	Leu	Phe	Met	Leu	Ser	Gly	Val	Pro	Asp	Ala	
		115					120					125				
Val	Phe	Asp	Leu	Thr	Asp	Leu	Asp	Val	Leu	Lys	Leu	Glu	Leu	Ile	Pro	
	130					135					140					
Glu	Ala	Lys	Ile	Pro	Ala	Lys	Ile	Ser	Gln	Met	Thr	Asn	Leu	Gln	Glu	
145					150					155					160	
Leu	His	Leu	Cys	His	Cys	Pro	Ala	Lys	Val	Glu	Gln	Thr	Ala	Phe	Ser	
				165					170					175		
Phe	Leu	Arg	Asp	His	Leu	Arg	Cys	Leu	His	Val	Lys	Phe	Thr	Asp	Val	
			180					185					190			



Ala	Glu	Ile	Pro	Ala	Trp	Val	Tyr	Leu	Leu	Lys	Asn	Leu	Arg	Glu	Leu	
	195						200								205	
Tyr	Leu	Ile	Gly	Asn	Leu	Asn	Ser	Glu	Asn	Asn	Lys	Met	Ile	Gly	Leu	
	210					215					220					
Glu	Ser	Leu	Arg	Glu	Leu	Arg	His	Leu	Lys	Ile	Leu	His	Val	Lys	Ser	
225					230					235					240	
Asn	Leu	Thr	Lys	Val	Pro	Ser	Asn	Ile	Thr	Asp	Val	Ala	Pro	His	Leu	
				245					250					255		
Thr	Lys	Leu	Val	Ile	His	Asn	Asp	Gly	Thr	Lys	Leu	Leu	Val	Leu	Asn	
			260					265					270			
Ser	Leu	Lys	Lys	Met	Met	Asn	Val	Ala	Glu	Leu	Glu	Leu	Gln	Asn	Cys	
	275						280					285				
Glu	Leu	Glu	Arg	Ile	Pro	His	Ala	Ile	Phe	Ser	Leu	Ser	Asn	Leu	Gln	
	290					295					300					
Glu	Leu	Asp	Leu	Lys	Ser	Asn	Asn	Ile	Arg	Thr	Ile	Glu	Glu	Ile	Ile	
305					310					315					320	
Ser	Phe	Gln	His	Leu	Lys	Arg	Leu	Thr	Cys	Leu	Lys	Leu	Trp	His	Asn	
				325					330					335		
Lys	Ile	Val	Thr	Ile	Pro	Pro	Ser	Ile	Thr	His	Val	Lys	Asn	Leu	Glu	
			340					345					350			
Ser	Leu	Tyr	Phe	Ser	Asn	Asn	Lys	Leu	Glu	Ser	Leu	Pro	Val	Ala	Val	
	355						360					365				
Phe	Ser	Leu	Gln	Lys	Leu	Arg	Cys	Leu	Asp	Val	Ser	Tyr	Asn	Asn	Ile	
	370					375					380					
Ser	Met	Ile	Pro	Ile	Glu	Ile	Gly	Leu	Leu	Gln	Asn	Leu	Gln	His	Leu	
385					390					395					400	
His	Ile	Thr	Gly	Asn	Lys	Val	Asp	Ile	Leu	Pro	Lys	Gln	Leu	Phe	Lys	
				405					410					415		
Cys	Ile	Lys	Leu	Arg	Thr	Leu	Asn	Leu	Gly	Gln	Asn	Cys	Ile	Thr	Ser	
			420					425					430			
Leu	Pro	Glu	Lys	Val	Gly	Gln	Leu	Ser	Gln	Leu	Thr	Gln	Leu	Glu	Leu	
	435						440					445				
Lys	Gly	Asn	Cys	Leu	Asp	Arg	Leu	Pro	Ala	Gln	Leu	Gly	Gln	Cys	Arg	
	450					455					460					
Met	Leu	Lys	Lys	Ser	Gly	Leu	Val	Val	Glu	Asp	His	Leu	Phe	Asp	Thr	



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<400> 189
cccacgcgctc cggcctttctc tctggacttt gcattttccat tcctttttcat tgacaaaactg 60
actttttttta tttcttttttt tccatctctg ggccagcttg ggatcctagg ccgccctggg 120
aagacatttg tgttttacac acataaggat ctgtgttttg ggtttcttct tcctccctg 180
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<210> 190
<211> 607
<212> PRT
<213> Homo sapiens
<400> 190
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Met	Glu	Leu	Val	Arg	Arg	Leu	Met	Pro	Leu	Thr	Leu	Leu	Ile	Leu	Ser
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Cys	Leu	Ala	Glu	Leu	Thr	Met	Ala	Glu	Ala	Glu	Gly	Asn	Ala	Ser	Cys
			20					25					30		
Thr	Val	Ser	Leu	Gly	Gly	Ala	Asn	Met	Ala	Glu	Thr	His	Lys	Ala	Met
		35					40					45			
Ile	Leu	Gln	Leu	Asn	Pro	Ser	Glu	Asn	Cys	Thr	Trp	Thr	Ile	Glu	Arg
	50					55					60				
Pro	Glu	Asn	Lys	Ser	Ile	Arg	Ile	Ile	Phe	Ser	Tyr	Val	Gln	Leu	Asp
65					70					75					80
Pro	Asp	Gly	Ser	Cys	Glu	Ser	Glu	Asn	Ile	Lys	Val	Phe	Asp	Gly	Thr
				85					90					95	
Ser	Ser	Asn	Gly	Pro	Leu	Leu	Gly	Gln	Val	Cys	Ser	Lys	Asn	Asp	Tyr
			100					105					110		
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	130					135					140				
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Leu	Glu	Gly	Ser	Phe	Thr	Ser	Pro	Asn	Tyr	Pro	Lys	Pro	His	Pro	Glu
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			180					185					190		
Lys	Leu	Asn	Phe	Lys	Glu	Ile	Phe	Leu	Glu	Ile	Asp	Lys	Gln	Cys	Lys
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Asn	Ser	Leu	Thr	Val	Val	Leu	Ser	Thr	Asp	Tyr	Ala	Asn	Ser	Tyr	Arg
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Thr	Ser	Leu	Thr	Cys	Ser	Ser	Asp	Arg	Met	Arg	Val	Ile	Ile	Ser	Lys
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Ser	Tyr	Leu	Glu	Ala	Phe	Asn	Ser	Asn	Gly	Asn	Asn	Leu	Gln	Leu	Lys
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Pro	Leu	Asn	Gly	Cys	Gly	Thr	Ile	Arg	Lys	Val	Glu	Asp	Gln	Ser	Ile
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			340					345					350		
Ile	Thr	Arg	Gln	Lys	Gln	Leu	Gln	Ile	Ile	Val	Lys	Cys	Glu	Met	Gly
		355					360					365			
His	Asn	Ser	Thr	Val	Glu	Ile	Ile	Tyr	Ile	Thr	Glu	Asp	Asp	Val	Ile
	370					375					380				
Gln	Ser	Gln	Asn	Ala	Leu	Gly	Lys	Tyr	Asn	Thr	Ser	Met	Ala	Leu	Phe
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Glu	Ser	Asn	Ser	Phe	Glu	Lys	Thr	Ile	Leu	Glu	Ser	Pro	Tyr	Tyr	Val
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Asp	Leu	Asn	Gln	Thr	Leu	Phe	Val	Gln	Val	Ser	Leu	His	Thr	Ser	Asp
			420					425					430		
Pro	Asn	Leu	Val	Val	Phe	Leu	Asp	Thr	Cys	Arg	Ala	Ser	Pro	Thr	Ser
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Asp	Phe	Ala	Ser	Pro	Thr	Tyr	Asp	Leu	Ile	Lys	Ser	Gly	Cys	Ser	Arg
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Asp	Glu	Thr	Cys	Lys	Val	Tyr	Pro	Leu	Phe	Gly	His	Tyr	Gly	Arg	Phe
465					470					475					480
Gln	Phe	Asn	Ala	Phe	Lys	Phe	Leu	Arg	Ser	Met	Ser	Ser	Val	Tyr	Leu
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Asn	Gln	Gly	Cys	Val	Ser	Arg	Ser	Lys	Arg	Asp	Ile	Ser	Ser	Tyr	Lys
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Trp	Lys	Thr	Asp	Ser	Ile	Ile	Gly	Pro	Ile	Arg	Leu	Lys	Arg	Asp	Arg
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Ser	Ala	Ser	Gly	Asn	Ser	Gly	Phe	Gln	His	Glu	Thr	His	Ala	Glu	Glu
545					550					555					560
Thr	Pro	Asn	Gln	Pro	Phe	Asn	Ser	Val	His	Leu	Phe	Ser	Phe	Met	Val



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Val	Asn	Gln	Arg	Ala	Asp	Tyr	Lys	Tyr	Gln	Lys	Leu	Gln	Asn	Tyr
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oligonucleotide probe

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<212> DNA
<213> Artificial Sequence
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<212> DNA
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ctgctgctgc cgccgcgcgc gtgccctgcc cacagcgcca cgcgcttcga ccccacctgg 180
```



gagtccttgg acgcccgcga gctgcccgcg tggtttgacc aggccaagtt cggcatcttc 240  
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 ctgtactatt ccctttttga atggtttcat ccgctcttcc ttgaggatga atccagttca 660  
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 gatcggtata acccaggaca tcttttgcca cataaatggg aaaactgcat gacaatagac 960  
 aaactgtcct ggggctatag gaggaagct ggaatctctg actatcttac aattgaagaa 1020  
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 cccacactag atggcaccat ttctgtagtt tttgaggagc gactgaggca agtgggggtcc 1140  
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&lt;210&gt; 195

&lt;211&gt; 467

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&lt;213&gt; Homo sapiens

&lt;400&gt; 195

Met Arg Pro Gln Glu Leu Pro Arg Leu Ala Phe Pro Leu Leu Leu Leu

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Leu Leu Leu Leu Leu Pro Pro Pro Pro Cys Pro Ala His Ser Ala Thr

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Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala

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 145 150 155 160  
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 245 250 255  
 Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys His Gly  
 260 265 270  
 Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His Leu Leu Pro  
 275 280 285  
 His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu Ser Trp Gly Tyr  
 290 295 300  
 Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr Ile Glu Glu Leu Val  
 305 310 315 320  
 Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn  
 325 330 335

1987-10-10 10:00:00



<210> 198



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catctgaggt	gtttccctgg	ctctgaaggg	gtaggcacga	tggccaggtg	cttcagcctg	180	
gtgttgcttc	tcacttccat	ctggaccacg	aggctcctgg	tccaaggctc	tttgctgcca	240	
gaagagcttt	ccatccaggt	gtcatgcaga	attatgggga	tcacccttgt	gagcaaaaag	300	
gcgaaccagc	agctgaattt	cacagaagct	aaggaggcct	gtaggctgct	gggactaagt	360	
ttggccggca	aggaccaagt	tgaacagctc	ttgaaagcta	gctttgaaac	ttgcagctat	420	
ggctgggttg	gagatggatt	cgtggtcatc	tctaggatta	gccccaaacc	caagtgtggg	480	
aaaaatgggg	tgggtgtcct	gatttggaa	gttccagtga	gccgacagtt	tgacgcctat	540	
gtttacaact	catctgatac	ttggactaac	tcgtgcattc	cagaaattat	caccacccaa	600	
tgatcccatat	tcaacactca	aactgcaaca	caaacaacag	aatttattgt	cagtgcagct	660	
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gccaatgata	gcaaccctaa	tgagggaatca	aagaaaactg	ataaaaaacc	agaagagtc	1080	
aagagtccaa	gcaaaactac	cgtgcgactg	ctggaagctg	aagtttagat	gagacagaaa	1140	
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atcaaaaggc	ccaaagaacc	aaagaagaaa	gtccaccctt	ggttcctaac	tggaatcagc	1260	
tcaggactgg	cattggacta	tggagtgcac	caaagagaat	gcccttctcc	ttattgtaac	1320	
cctgtctgga	tcctatcctc	ctacctccaa	agcttcccac	ggcctttcta	gcctggctat	1380	
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<210> 201
<211> 322
<212> PRT
<213> Artificial sequence
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<400> 201

Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala Glu Glu Leu Ser Ile  
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Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala  
35 40 45

Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu  
50 55 60

Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala  
65 70 75 80

Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val  
85 90 95

Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly  
100 105 110

Val Leu Ile Trp Lys Val Pro Val Ser Arg Gln Phe Ala Ala Tyr Cys  
115 120 125

Tyr Asn Ser Ser Asp Thr Trp Thr Asn Ser Cys Ile Pro Glu Ile Ile  
130 135 140



```
<210> 203
<211> 22
<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

gtcagtgaca gtacctactc gg

22

<211> 24

<212> DNA

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

tggagcagga ggagtagtag tagg

24

<211> 50

<212> DNA

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 205  
aggaggcctg taggctgctg ggactaagtt tggccggcaa ggaccaagtt

50

<211> 1620

<212> DNA

<213> Homo sapiens

<221> modified base

<222> (973)

<223> a, t, c or g

<221> modified base

<222> (977)

<223> a, t, c or g

<221> modified\_base

<222> (996)

<223> a, t, c or g

```
<221> modified_base
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&lt;222&gt; (1003)

&lt;223&gt; a, t, c or g

&lt;400&gt; 206

```

agatggcggg cttggcacct ctaattgctc tcgtgtattc ggtgccgcga ctttcacgat 60
ggctcgccca accttactac cttctgtcgg ccctgctctc tgctgccttc ctactcgtga 120
ggaaactgcc gccgctctgc cacggtctgc ccaccaacg cgaagacggg aaccctgtgt 180
actttgactg gagagaagtg gagatcctga tgtttctcag tgccattgtg atgatgaaga 240
accgcagatc catcactgtg gagcaacata taggcaacat tttcatgttt agtaaagtgg 300
ccaacacaat tcttttcttc cgcttggata ttcgcatggg cctactttac atcacactct 360
gcatagtgtt cctgatgacg tgcaaaccct ccctatatat gggccctgag tatatcaagt 420
acttcaatga taaaaccatt gatgaggaac tagaacggga caagaggggc acttggattg 480
tggagtctct tgccaattgg tctaagtact gccaatcatt tgccctatc tatgctgacc 540
tctcccttaa atacaactgt acagggctaa attttgggaa ggtggatgtt ggacgctata 600
ctgatgttag tacgcggtac aaagttagca catcacccct caccaagcaa ctccctaccc 660
tgatcctgtt ccaaggtggc aaggaggcaa tgccggcgcc acagattgac aagaaaggac 720
gggctgtctc atggaccttc tctgaggaga atgtgatccg agaatttaac ttaaattgagc 780
tataccagcg ggccaagaaa ctatcaaagg ctggagacaa tatccctgag gaggagcctg 840
tggttcaaac ccccaccaca gtgtcagatg gggaaaacaa gaaggataaa taagatcctc 900
actttggcag tgcttctctt cctgtcaatt ccaggctctt tccataacca caagcctgag 960
gctgcagcct ttnattnatg ttttcccttt ggctgngact ggntggggca gcatgcagct 1020
tctgatttta aagaggcatc tagggaattg tcaggcaccc tacaggaagg cctgccatgc 1080
tgtggccaac tgtttactc gagcaagaaa gagatctcat aggacggagg gggaaatggt 1140
ttccctccaa gcttgggtca gtgtgttaac tgcttatcag ctattcagac atctccatgg 1200
tttctccatg aaactctgtg gtttcatcat tccttcttag ttgacctgca cagcttgggt 1260
agacctagat ttaaccctaa ggtaagatgc tggggtatag aacgctaaga attttcccc 1320
aaggactctt gcttccttaa gcccttctgg cttcgtttat ggtcttcatt aaaagtataa 1380
gcctaacttt gtcgctagtc ctaaggagaa acctttaacc acaaagtttt tatcattgaa 1440
gacaatattg aacaaccccc tattttgtgg ggattgagaa ggggtgaata gaggcttgag 1500
actttccttt gtgtggtagg acttggagga gaaatccctt ggactttcac taaccctctg 1560
acatactccc cacaccagat tgatggcttt ccgtaataaa aagattggga tttccttttg 1620

```

&lt;210&gt; 207

&lt;211&gt; 296

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 207

```

Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg
  1              5              10              15

```

```

Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu
          20              25              30

```

```

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly
          35              40              45

```

```

Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg
          50              55              60

```

```

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn
          65              70              75              80

```

F00140.206.1



gcttggatat tcgcatgggc ctac



<400>	212						
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cccattgctc	ctgctgcccg	gctcctacgg	actgcccttc	tacaacggct	tctactactc	180	
caacagcgcc	aacgaccaga	acctaggcaa	cggctcatggc	aaagaccttc	ttaatggagt	240	
gaagctggtg	gtggagacac	ccgaggagac	cctgttcacc	taccaagggg	ccagtgtgat	300	
cctgccctgc	cgctaccgct	acgagccggc	cctggctctcc	ccgcggcgctg	tgcgtgtcaa	360	
atggtggaag	ctgtcggaga	acggggcccc	agagaaggac	gtgctggtgg	ccatcgggct	420	
gaggcacccg	tcctttgggg	actaccaagg	ccgcgtgcac	ctgcggcagg	acaaagagca	480	
tgacgtctcg	ctggagatcc	aggatctgcg	gctggaggac	tatgggcgtt	accgctgtga	540	
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```
<210> 213
<211> 360
<212> PRT
<213> Homo sapiens
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<400> 213
Met Gly Leu Leu Leu Leu Val Pro Leu Leu Leu Leu Pro Gly Ser Tyr
  1               5               10               15
Gly Leu Pro Phe Tyr Asn Gly Phe Tyr Tyr Ser Asn Ser Ala Asn Asp
  20               25               30
Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Leu Asn Gly Val Lys
  35               40               45
Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr Tyr Gln Gly Ala
  50               55               60
Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser
  65               70               75               80
Pro Arg Arg Val Arg Val Lys Trp Trp Lys Leu Ser Glu Asn Gly Ala
  85               90               95
Pro Glu Lys Asp Val Leu Val Ala Ile Gly Leu Arg His Arg Ser Phe
 100               105               110
Gly Asp Tyr Gln Gly Arg Val His Leu Arg Gln Asp Lys Glu His Asp

```



```
<210> 214
<211> 18
<212> DNA
<213> Artificial Sequence
<220>
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<400> 218  
tqtccaaagt acacacacct gagg 24



<210> 219  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 219  
 gatgccacga tcgccaaggt gggacagctc tttgccgcct ggaag 45

<210> 220  
 <211> 1503  
 <212> DNA  
 <213> Homo sapiens

<400> 220  
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 gcttctgttg ctactgaggg acggggccca ggggaagcca tccccagacg caggccctca 120  
 tggccagggg aggggtgcacc aggcggcccc cctgagcgac gctcccatg atgacgcca 180  
 cgggaacttc cagtacgacc atgaggcttt cctgggacgg gaagtggcca aggaattcga 240  
 ccaactcacc ccagaggaaa gccaggcccc tctggggcgg atcgtggacc gcatggaccg 300  
 cgcgggggac ggcgacggct ggggtgtcgt ggccgagctt cgcgcgtgga tcgcgcacac 360  
 gcagcagcgg cacatacggg actcgggtgag cgcggcctgg gacacgtacg acacggaccg 420  
 cgacgggcgt gtgggttggg aggagctgcg caacgccacc tatggccact acgcgcccgg 480  
 tgaagaattt catgacgtgg aggatgcaga gacctacaaa aagatgctgg ctcgggacga 540  
 gcggcgcttc cgggtggccg accaggatgg ggactcgatg gccactcgag aggagctgac 600  
 agccttcctg cccccgagg agttccctca catgcgggac atcgtgattg ctgaaaccct 660  
 ggaggacctg gacagaaaca aagatggcta tgtccagggtg gaggagtaca tcgcggtatc 720  
 gtactcagcc gagcctgggg aggaggagcc ggcgtgggtg cagacggaga ggcagcagtt 780  
 ccgggacttc cgggatctga acaaggatgg gcacctggat gggagtgagg tgggccactg 840  
 ggtgctgccc cctgcccagg accagcccct ggtggaagcc aaccacctgc tgcacgagag 900  
 cgacacggac aaggatgggc ggctgagcaa agcggaaatc ctgggtaatt ggaacatgtt 960  
 tgtgggcagt caggccacca actatggcga ggacctgacc cggcaccacg atgagctgtg 1020  
 agcaccgcgc acctgccaca gcctcagagg ccgcacaaat gaccggagga ggggcccgtg 1080  
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 cagctccaaa tctgagcctc caccacatag actgaaactc ccctggcccc agccctctcc 1380  
 tgcttggeet ggctgggac acctcctctc tgccaggagg caataaaagc cagcgccggg 1440  
 accttgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500  
 aaa 1503

<210> 221  
 <211> 328  
 <212> PRT  
 <213> Homo sapiens

<400> 221  
 Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg His

TC2120103066



[illegible]



<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe



44

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<210> 226
<211> 2403
<212> DNA
<213> Homo sapiens
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gggcggcggg	cgcgggtgcg	agggatccct	gacgcctctg	tccttgtttc	tttgtcgctc	120	
ccagcctgtc	tgtcgtcgtt	ttggcgcccc	cgcctccccg	cggtgcgggg	ttgcacaccg	180	
atcctgggct	tcgctcgatt	tgccgcgcag	gcgcctccca	gacctagagg	ggcgctggcc	240	
tggagcagcg	ggtcgtctgt	gtcctctctc	ctctgcgcgc	cgcccgggga	tccgaagggt	300	
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cctctctccc	aggtgtgagc	agcctatcag	tcaccatgtc	cgcagcctgg	atcccggctc	420	
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tgattgatgg	aagctttaat	attgggcagc	gccagattta	tttacagaag	aattttgttg	960	
gaaaagtggc	tctaattgtt	ggaattggaa	cagaaggacc	acatgtgggc	cttgttcaag	1020	
ccagtgaaca	tcccaaaata	gaattttact	tgaaaaactt	tacatcagcc	aaagatgttt	1080	
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ccagagagtt	tggtgtcaat	gtatttatag	tttctgtggc	caagcctatc	cctgaagaac	1320	
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atgtcctagc	tgctcatcaga	aacatccgct	atatgagtg	tggaacagct	actggtgatg	1740	
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gattagaacc	aattgtttct	gatgtcatca	gaggcatttg	tagagatttc	ttagaatccc	2040	
agcaataatg	gtaacatttt	gacaactgaa	agaaaaagta	caaggggatc	cagtggttaa	2100	
attgtattct	cataatactg	aaatgcttta	gcatactaga	atcagatata	aaactattaa	2160	
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aatttacagt	gtactttggt	aaaaacactg	ctgaggcttc	ataatcatgg	ctcttagaaa	2280	
ctcaggaag	aggagataat	gtggattaaa	accttaagag	ttctaaccat	gcctactaaa	2340	
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aaa						2403	

<210> 227



<400> 227

Met Ser Ala Ala Trp Ile Pro Ala Leu Gly Leu Gly Val Cys Leu Leu  
1 5 10 15

Leu Leu Pro Gly Pro Ala Gly Ser Glu Gly Ala Ala Pro Ile Ala Ile  
20 25 30

Thr Cys Phe Thr Arg Gly Leu Asp Ile Arg Lys Glu Lys Ala Asp Val  
35 40 45

Leu Cys Pro Gly Gly Cys Pro Leu Glu Glu Phe Ser Val Tyr Gly Asn  
50 55 60

Ile Val Tyr Ala Ser Val Ser Ser Ile Cys Gly Ala Ala Val His Arg  
65 70 75 80

Gly Val Ile Ser Asn Ser Gly Gly Pro Val Arg Val Tyr Ser Leu Pro  
85 90 95

Gly Arg Glu Asn Tyr Ser Ser Val Asp Ala Asn Gly Ile Gln Ser Gln  
100 105 110

Met Leu Ser Arg Trp Ser Ala Ser Phe Thr Val Thr Lys Gly Lys Ser  
115 120 125

Ser Thr Gln Glu Ala Thr Gly Gln Ala Val Ser Thr Ala His Pro Pro  
130 135 140

Thr Gly Lys Arg Leu Lys Lys Thr Pro Glu Lys Lys Thr Gly Asn Lys  
145 150 155 160

Asp Cys Lys Ala Asp Ile Ala Phe Leu Ile Asp Gly Ser Phe Asn Ile  
165 170 175

Gly Gln Arg Arg Phe Asn Leu Gln Lys Asn Phe Val Gly Lys Val Ala  
180 185 190

Leu Met Leu Gly Ile Gly Thr Glu Gly Pro His Val Gly Leu Val Gln  
195 200 205

Ala Ser Glu His Pro Lys Ile Glu Phe Tyr Leu Lys Asn Phe Thr Ser  
210 215 220

Ala Lys Asp Val Leu Phe Ala Ile Lys Glu Val Gly Phe Arg Gly Gly  
225 230 235 240

Asn Ser Asn Thr Gly Lys Ala Leu Lys His Thr Ala Gln Lys Phe Phe  
245 250 255



Thr Val Asp Ala Gly Val Arg Lys Gly Ile Pro Lys Val Val Val  
260 265 270

Phe Ile Asp Gly Trp Pro Ser Asp Asp Ile Glu Glu Ala Gly Ile Val  
275 280 285

Ala Arg Glu Phe Gly Val Asn Val Phe Ile Val Ser Val Ala Lys Pro  
290 295 300

Ile Pro Glu Glu Leu Gly Met Val Gln Asp Val Thr Phe Val Asp Lys  
305 310 315 320

Ala Val Cys Arg Asn Asn Gly Phe Phe Ser Tyr His Met Pro Asn Trp  
325 330 335

Phe Gly Thr Thr Lys Tyr Val Lys Pro Leu Val Gln Lys Leu Cys Thr  
340 345 350

His Glu Gln Met Met Cys Ser Lys Thr Cys Tyr Asn Ser Val Asn Ile  
355 360 365

Ala Phe Leu Ile Asp Gly Ser Ser Ser Val Gly Asp Ser Asn Phe Arg  
370 375 380

Leu Met Leu Glu Phe Val Ser Asn Ile Ala Lys Thr Phe Glu Ile Ser  
385 390 395 400

Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr Asp Gln Arg  
405 410 415

Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala  
420 425 430

Val Ile Arg Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala Thr Gly Asp  
435 440 445

Ala Ile Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg Glu Ser  
450 455 460

Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp  
465 470 475 480

Asp Val Gln Gly Pro Ala Ala Ala Ala His Asp Ala Gly Ile Thr Ile  
485 490 495

Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Lys Asp Met  
500 505 510

Ala Ser Lys Pro Lys Glu Ser His Ala Phe Phe Thr Arg Glu Phe Thr  
515 520 525

Gly Leu Glu Pro Ile Val Ser Asp Val Ile Arg Gly Ile Cys Arg Asp  
530 535 540



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<210> 228
<211> 18
<212> DNA
<213> Artificial Sequence
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<400> 228	18
tggtctcgca caccgatc	

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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<210> 230
<211> 18
<212> DNA
<213> Artificial Sequence
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<400> 230 18  
ccttgaagca tactgctc

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<210> 232



<400> 235						
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gtcggggcgg	cggctgcggg	cgcagagcgg	agatgcagcg	gcttggggcc	accctgctgt	180
gcctgtgtct	ggcgggcgcg	gtccccacgg	cccccgcgcc	cgctccgacg	gcgacctcgg	240
ctccagtc aa	gccccggccc	gctctcagct	acccgcagga	ggaggccacc	ctcaatgaga	300
tgttccgcga	ggttgaggaa	ctgatggagg	acacgcagca	caaattgcgc	agcgcggtgg	360
aagagatgga	ggcagaagaa	gctgtgtcta	aagcatcatc	agaagtgaac	ctggcaaact	420
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<210> 236
<211> 350
<212> PRT
<213> Homo sapiens
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<400> 236
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Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val
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Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn
      35                               40                      45

Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
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Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
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<210> 237



17

49

24

18

18



24

45

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gcctgggtga cagaatgaga ctctgtctca aacaaacaaa cacgggagga 600
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<210> 245

<211> 713

<212> PRT

<213> Homo Sapien

<400> 245

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Pro	Gln	Cys	Ala	Cys	Gln	Ile	Arg	Pro	Trp	Tyr	Thr	Pro	Arg	Ser	35	40	45	
Ser	Tyr	Arg	Glu	Ala	Thr	Thr	Val	Asp	Cys	Asn	Asp	Leu	Phe	Leu	50	55	60	
Thr	Ala	Val	Pro	Pro	Ala	Leu	Pro	Ala	Gly	Thr	Gln	Thr	Leu	Leu	65	70	75	
Leu	Gln	Ser	Asn	Ser	Ile	Val	Arg	Val	Asp	Gln	Ser	Glu	Leu	Gly	80	85	90	
Tyr	Leu	Ala	Asn	Leu	Thr	Glu	Leu	Asp	Leu	Ser	Gln	Asn	Ser	Phe	95	100	105	
Ser	Asp	Ala	Arg	Asp	Cys	Asp	Phe	His	Ala	Leu	Pro	Gln	Leu	Leu	110	115	120	
Ser	Leu	His	Leu	Glu	Glu	Asn	Gln	Leu	Thr	Arg	Leu	Glu	Asp	His	125	130	135	
Ser	Phe	Ala	Gly	Leu	Ala	Ser	Leu	Gln	Glu	Leu	Tyr	Leu	Asn	His	140	145	150	

09090410200660



Asn	Gln	Leu	Tyr	Arg	Ile	Ala	Pro	Arg	Ala	Phe	Ser	Gly	Leu	Ser	
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				170					175					180	
Asp	Ser	Arg	Trp	Phe	Glu	Met	Leu	Pro	Asn	Leu	Glu	Ile	Leu	Met	
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Ile	Gly	Gly	Asn	Lys	Val	Asp	Ala	Ile	Leu	Asp	Met	Asn	Phe	Arg	
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Pro	Leu	Ala	Asn	Leu	Arg	Ser	Leu	Val	Leu	Ala	Gly	Met	Asn	Leu	
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Arg	Glu	Ile	Ser	Asp	Tyr	Ala	Leu	Glu	Gly	Leu	Gln	Ser	Leu	Glu	
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Ser	Leu	Ser	Phe	Tyr	Asp	Asn	Gln	Leu	Ala	Arg	Val	Pro	Arg	Arg	
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Asn	Pro	Leu	Gln	Arg	Val	Gly	Pro	Gly	Asp	Phe	Ala	Asn	Met	Leu	
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Ile	Asp	Lys	Phe	Ala	Leu	Val	Asn	Leu	Pro	Glu	Leu	Thr	Lys	Leu	
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Phe	His	His	Leu	Pro	Gln	Met	Glu	Thr	Leu	Met	Leu	Asn	Asn	Asn	
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Leu	Gln	Glu	Val	Gly	Leu	His	Gly	Asn	Pro	Ile	Arg	Cys	Asp	Cys	
				365					370					375	
Val	Ile	Arg	Trp	Ala	Asn	Ala	Thr	Gly	Thr	Arg	Val	Arg	Phe	Ile	
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Glu	Pro	Gln	Ser	Thr	Leu	Cys	Ala	Glu	Pro	Pro	Asp	Leu	Gln	Arg	
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Leu	Pro	Val	Arg	Glu	Val	Pro	Phe	Arg	Glu	Met	Thr	Asp	His	Cys	



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				425						430					435		
Ala	Ser	Gly	Glu	Ser	Met	Val	Leu	His		Cys	Arg	Ala	Leu	Ala	Glu		
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Pro	Glu	Pro	Glu	Ile	Tyr	Trp	Val	Thr		Pro	Ala	Gly	Leu	Arg	Leu		
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Thr	Pro	Ala	His	Ala	Gly	Arg	Arg	Tyr		Arg	Val	Tyr	Pro	Glu	Gly		
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Thr	Leu	Glu	Leu	Arg	Arg	Val	Thr	Ala		Glu	Glu	Ala	Gly	Leu	Tyr		
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Thr	Cys	Val	Ala	Gln	Asn	Leu	Val	Gly		Ala	Asp	Thr	Lys	Thr	Val		
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Ser	Val	Val	Val	Gly	Arg	Ala	Leu	Leu		Gln	Pro	Gly	Arg	Asp	Glu		
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Gly	Gln	Gly	Leu	Glu	Leu	Arg	Val	Gln		Glu	Thr	His	Pro	Tyr	His		
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Ile	Leu	Leu	Ser	Trp	Val	Thr	Pro	Pro		Asn	Thr	Val	Ser	Thr	Asn		
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Leu	Thr	Trp	Ser	Ser	Ala	Ser	Ser	Leu		Arg	Gly	Gln	Gly	Ala	Thr		
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Ala	Leu	Ala	Arg	Leu	Pro	Arg	Gly	Thr		His	Ser	Tyr	Asn	Ile	Thr		
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Arg	Leu	Leu	Gln	Ala	Thr	Glu	Tyr	Trp		Ala	Cys	Leu	Gln	Val	Ala		
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Phe	Ala	Asp	Ala	His	Thr	Gln	Leu	Ala		Cys	Val	Trp	Ala	Arg	Thr		
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Lys	Glu	Ala	Thr	Ser	Cys	His	Arg	Ala		Leu	Gly	Asp	Arg	Pro	Gly		
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Leu	Ala	Ala	His	Leu	Gly	Thr	Gly	Gln		Pro	Arg	Lys	Gly	Val	Gly		
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Gly	Arg	Arg	Pro	Leu	Pro	Pro	Ala	Trp		Ala	Phe	Trp	Gly	Trp	Ser		
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<210> 250

<211> 546

<212> PRT

<213> Homo Sapien

<400> 250

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400> 250
Met Arg Gln Thr Ile Ile Lys Val Ile Lys Phe Ile Leu Ile Ile
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Cys Tyr Thr Val Tyr Tyr Val His Asn Ile Lys Phe Asp Val Asp  
20 25 30

Cys Thr Val Asp Ile Glu Ser Leu Thr Gly Tyr Arg Thr Tyr Arg  
35 40 45

Cys Ala His Pro Leu Ala Thr Leu Phe Lys Ile Leu Ala Ser Phe  
50 55 60

Tyr Ile Ser Leu Val Ile Phe Tyr Gly Leu Ile Cys Met Tyr Thr  
65 70 75

Leu Trp Trp Met Leu Arg Arg Ser Leu Lys Lys Tyr Ser Phe Glu  
80 85 90

Ser Ile Arg Glu Glu Ser Ser Tyr Ser Asp Ile Pro Asp Val Lys



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Asn	Asp	Phe	Ala	Phe	Met	Leu	His	Leu	Ile	Asp	Gln	Tyr	Asp	Pro					
				110					115					120					
Leu	Tyr	Ser	Lys	Arg	Phe	Ala	Val	Phe	Leu	Ser	Glu	Val	Ser	Glu					
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Asn	Lys	Leu	Arg	Gln	Leu	Asn	Leu	Asn	Asn	Glu	Trp	Thr	Leu	Asp					
				140					145					150					
Lys	Leu	Arg	Gln	Arg	Leu	Thr	Lys	Asn	Ala	Gln	Asp	Lys	Leu	Glu					
				155					160					165					
Leu	His	Leu	Phe	Met	Leu	Ser	Gly	Ile	Pro	Asp	Thr	Val	Phe	Asp					
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Leu	Val	Glu	Leu	Glu	Val	Leu	Lys	Leu	Glu	Leu	Ile	Pro	Asp	Val					
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Thr	Ile	Pro	Pro	Ser	Ile	Ala	Gln	Leu	Thr	Gly	Leu	Lys	Glu	Leu					
				200					205					210					
Trp	Leu	Tyr	His	Thr	Ala	Ala	Lys	Ile	Glu	Ala	Pro	Ala	Leu	Ala					
				215					220					225					
Phe	Leu	Arg	Glu	Asn	Leu	Arg	Ala	Leu	His	Ile	Lys	Phe	Thr	Asp					
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Ile	Lys	Glu	Ile	Pro	Leu	Trp	Ile	Tyr	Ser	Leu	Lys	Thr	Leu	Glu					
				245					250					255					
Glu	Leu	His	Leu	Thr	Gly	Asn	Leu	Ser	Ala	Glu	Asn	Asn	Arg	Tyr					
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Ile	Val	Ile	Asp	Gly	Leu	Arg	Glu	Leu	Lys	Arg	Leu	Lys	Val	Leu					
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Arg	Leu	Lys	Ser	Asn	Leu	Ser	Lys	Leu	Pro	Gln	Val	Val	Thr	Asp					
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Val	Gly	Val	His	Leu	Gln	Lys	Leu	Ser	Ile	Asn	Asn	Glu	Gly	Thr					
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Lys	Leu	Ile	Val	Leu	Asn	Ser	Leu	Lys	Lys	Met	Ala	Asn	Leu	Thr					
				320					325					330					
Glu	Leu	Glu	Leu	Ile	Arg	Cys	Asp	Leu	Glu	Arg	Ile	Pro	His	Ser					
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Ile	Phe	Ser	Leu	His	Asn	Leu	Gln	Glu	Ile	Asp	Leu	Lys	Asp	Asn					
				350					355					360					



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 Pro Ile Gln Ile Gly Asn Leu Thr Asn Leu Glu Arg Leu Tyr Leu  
 395 400 405  
 Asn Arg Asn Lys Ile Glu Lys Ile Pro Thr Gln Leu Phe Tyr Cys  
 410 415 420  
 Arg Lys Leu Arg Tyr Leu Asp Leu Ser His Asn Asn Leu Thr Phe  
 425 430 435  
 Leu Pro Ala Asp Ile Gly Leu Leu Gln Asn Leu Gln Asn Leu Ala  
 440 445 450  
 Ile Thr Ala Asn Arg Ile Glu Thr Leu Pro Pro Glu Leu Phe Gln  
 455 460 465  
 Cys Arg Lys Leu Arg Ala Leu His Leu Gly Asn Asn Val Leu Gln  
 470 475 480  
 Ser Leu Pro Ser Arg Val Gly Glu Leu Thr Asn Leu Thr Gln Ile  
 485 490 495  
 Glu Leu Arg Gly Asn Arg Leu Glu Cys Leu Pro Val Glu Leu Gly  
 500 505 510  
 Glu Cys Pro Leu Leu Lys Arg Ser Gly Leu Val Val Glu Glu Asp  
 515 520 525  
 Leu Phe Asn Thr Leu Pro Pro Glu Val Lys Glu Arg Leu Trp Arg  
 530 535 540  
 Ala Asp Lys Glu Gln Ala  
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<210> 251

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 251

caacaatgag ggcaccaagc 20

<210> 252

<211> 24

09909304 074604



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<400> 254
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tgaacgcagg agctgtcatt gactggccca cagaggaggg caaggaagta 150
tgggattatg tgacggtccg caaggatgcc tacatgttct ggtggctcta 200
ttatgccacc aactcctgca agaacttctc agaactgccc ctggtcattgt 250
ggcttcaggg cggtccagge ggttctagca ctggatttg aaactttgag 300
gaaattgggc cccttgacag tgatctcaaa ccacggaaaa ccacctggct 350
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cagctggcat tggctagag ctttataagg ccattcagcg agggaccatc 600
aagtgcaact ttgcgggggt tgccttgggt gattcctgga tctcccctgt 650
tgattcggtg ctctcctggg gaccttacct gtacagcatg tctcttctcg 700

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aagacaaagg tctggcagag gtgtctaagg ttgcagagca agtactgaat 750  
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<210> 255

<211> 452

<212> PRT

<213> Homo Sapien

<400> 255

Met	Glu	Leu	Ala	Leu	Arg	Arg	Ser	Pro	Val	Pro	Arg	Trp	Leu	Leu
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Leu	Leu	Pro	Leu	Leu	Leu	Gly	Leu	Asn	Ala	Gly	Ala	Val	Ile	Asp
				20					25				30	

Trp	Pro	Thr	Glu	Glu	Gly	Lys	Glu	Val	Trp	Asp	Tyr	Val	Thr	Val
				35					40				45	



Arg	Lys	Asp	Ala	Tyr	Met	Phe	Trp	Trp	Leu	Tyr	Tyr	Ala	Thr	Asn	60
				50					55						
Ser	Cys	Lys	Asn	Phe	Ser	Glu	Leu	Pro	Leu	Val	Met	Trp	Leu	Gln	75
				65					70						
Gly	Gly	Pro	Gly	Gly	Ser	Ser	Thr	Gly	Phe	Gly	Asn	Phe	Glu	Glu	90
				80					85						
Ile	Gly	Pro	Leu	Asp	Ser	Asp	Leu	Lys	Pro	Arg	Lys	Thr	Thr	Trp	105
				95					100						
Leu	Gln	Ala	Ala	Ser	Leu	Leu	Phe	Val	Asp	Asn	Pro	Val	Gly	Thr	120
				110					115						
Gly	Phe	Ser	Tyr	Val	Asn	Gly	Ser	Gly	Ala	Tyr	Ala	Lys	Asp	Leu	135
				125					130						
Ala	Met	Val	Ala	Ser	Asp	Met	Met	Val	Leu	Leu	Lys	Thr	Phe	Phe	150
				140					145						
Ser	Cys	His	Lys	Glu	Phe	Gln	Thr	Val	Pro	Phe	Tyr	Ile	Phe	Ser	165
				155					160						
Glu	Ser	Tyr	Gly	Gly	Lys	Met	Ala	Ala	Gly	Ile	Gly	Leu	Glu	Leu	180
				170					175						
Tyr	Lys	Ala	Ile	Gln	Arg	Gly	Thr	Ile	Lys	Cys	Asn	Phe	Ala	Gly	195
				185					190						
Val	Ala	Leu	Gly	Asp	Ser	Trp	Ile	Ser	Pro	Val	Asp	Ser	Val	Leu	210
				200					205						
Ser	Trp	Gly	Pro	Tyr	Leu	Tyr	Ser	Met	Ser	Leu	Leu	Glu	Asp	Lys	225
				215					220						
Gly	Leu	Ala	Glu	Val	Ser	Lys	Val	Ala	Glu	Gln	Val	Leu	Asn	Ala	240
				230					235						
Val	Asn	Lys	Gly	Leu	Tyr	Arg	Glu	Ala	Thr	Glu	Leu	Trp	Gly	Lys	255
				245					250						
Ala	Glu	Met	Ile	Ile	Glu	Gln	Asn	Thr	Asp	Gly	Val	Asn	Phe	Tyr	270
				260					265						
Asn	Ile	Leu	Thr	Lys	Ser	Thr	Pro	Thr	Ser	Thr	Met	Glu	Ser	Ser	285
				275					280						
Leu	Glu	Phe	Thr	Gln	Ser	His	Leu	Val	Cys	Leu	Cys	Gln	Arg	His	300
				290					295						
Val	Arg	His	Leu	Gln	Arg	Asp	Ala	Leu	Ser	Gln	Leu	Met	Asn	Gly	



Gln Glu

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tggagaggac gccgaactcg ggcgttggcc gtggcagggg agcctgcgcc 200
tgtgggattc ccacgtatgc ggagtgagcc tgctcagcca ccgctgggca 250
ctcacggcgg cgcactgctt tgaaacctat agtgacctta gtgatccctc 300
cgggtggatg gtccagtttg gccagctgac ttccatgcca tccttctgga 350
gcctgcaggc ctactacacc cgttacttcg tatcgaatat ctatctgagc 400
```



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<210> 257
<211> 314
<212> PRT
<213> Homo Sapien
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```

<400> 257
Met Gly Ala Arg Gly Ala Leu Leu Leu Ala Leu Leu Leu Ala Arg
  1                      5                      10                      15

Ala Gly Leu Arg Lys Pro Glu Ser Gln Glu Ala Ala Pro Leu Ser
                      20                      25                      30

Gly Pro Cys Gly Arg Arg Val Ile Thr Ser Arg Ile Val Gly Gly
                      35                      40                      45

Glu Asp Ala Glu Leu Gly Arg Trp Pro Trp Gln Gly Ser Leu Arg
                      50                      55                      60

Leu Trp Asp Ser His Val Cys Gly Val Ser Leu Leu Ser His Arg
                      65                      70                      75

Trp Ala Leu Thr Ala Ala His Cys Phe Glu Thr Tyr Ser Asp Leu
                      80                      85                      90

```



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<210> 258
<211> 2427
<212> DNA
<213> Homo Sapien
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<400> 258  
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cggagcccga ccagcggagg acgctgcccc caggctgggt gtccctgggc 150  
cgtgcggaacc ctgaggaaga gctgagtctc acctttgccc tgagacagca 200  
gaatgtggaa agactctcgg agctggtgca ggctgtgtcg gatcccagct 250  
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aggccatccc cactgaccct ccacacgggtg caaaaatggc tcttggcagc 350  
cggagcccag aagtgccatt ctgtgatcac acaggacttt ctgacttgct 400  
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tgcaccgttt tcccccaaca tcctccctga ggcaacgtcc tgagccgcag 600  
gtgacaggga ctgtaggcct gcctctgggg gtaacccct ctgtgatccg 650  
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acagccaagc ctgtgccag ttctggagc agtatttcca tgactcagac 750  
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cgcctcaggt gacagtgggg ccgggtgttg gtctgtctct ggaagacacc 1150  
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ggcacatcct tccaggaacc ttctctatc acaaataaaa ttgttgacta 1250  
tatcagtggg ggtggcttca gcaatgtgtt cccacggcct tcataccagg 1300  
aggaagctgt aacgaagttc ctgagctcta gccccacct gccaccatcc 1350  
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<210> 259
<211> 556
<212> PRT
<213> Homo Sapien
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<400> 259
Met Gly Leu Gln Ala Cys Leu Leu Gly Leu Phe Ala Leu Ile Leu
  1                               5          10          15

Ser Gly Lys Cys Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr

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	20		25		30
Leu Pro Pro Gly Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu	35		40		45
Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg	50		55		60
Leu Ser Glu Leu Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln	65		70		75
Tyr Gly Lys Tyr Leu Thr Leu Glu Asn Val Ala Asp Leu Val Arg	80		85		90
Pro Ser Pro Leu Thr Leu His Thr Val Gln Lys Trp Leu Leu Ala	95		100		105
Ala Gly Ala Gln Lys Cys His Ser Val Ile Thr Gln Asp Phe Leu	110		115		120
Thr Cys Trp Leu Ser Ile Arg Gln Ala Glu Leu Leu Leu Pro Gly	125		130		135
Ala Glu Phe His His Tyr Val Gly Gly Pro Thr Glu Thr His Val	140		145		150
Val Arg Ser Pro His Pro Tyr Gln Leu Pro Gln Ala Leu Ala Pro	155		160		165
His Val Asp Phe Val Gly Gly Leu His Arg Phe Pro Pro Thr Ser	170		175		180
Ser Leu Arg Gln Arg Pro Glu Pro Gln Val Thr Gly Thr Val Gly	185		190		195
Leu His Leu Gly Val Thr Pro Ser Val Ile Arg Lys Arg Tyr Asn	200		205		210
Leu Thr Ser Gln Asp Val Gly Ser Gly Thr Ser Asn Asn Ser Gln	215		220		225
Ala Cys Ala Gln Phe Leu Glu Gln Tyr Phe His Asp Ser Asp Leu	230		235		240
Ala Gln Phe Met Arg Leu Phe Gly Gly Asn Phe Ala His Gln Ala	245		250		255
Ser Val Ala Arg Val Val Gly Gln Gln Gly Arg Gly Arg Ala Gly	260		265		270
Ile Glu Ala Ser Leu Asp Val Gln Tyr Leu Met Ser Ala Gly Ala	275		280		285

FOOTNOTES



Asn	Ile	Ser	Thr	Trp	Val	Tyr	Ser	Ser	Pro	Gly	Arg	His	Glu	Gly
				290					295					300
Gln	Glu	Pro	Phe	Leu	Gln	Trp	Leu	Met	Leu	Leu	Ser	Asn	Glu	Ser
				305					310					315
Ala	Leu	Pro	His	Val	His	Thr	Val	Ser	Tyr	Gly	Asp	Asp	Glu	Asp
				320					325					330
Ser	Leu	Ser	Ser	Ala	Tyr	Ile	Gln	Arg	Val	Asn	Thr	Glu	Leu	Met
				335					340					345
Lys	Ala	Ala	Ala	Arg	Gly	Leu	Thr	Leu	Leu	Phe	Ala	Ser	Gly	Asp
				350					355					360
Ser	Gly	Ala	Gly	Cys	Trp	Ser	Val	Ser	Gly	Arg	His	Gln	Phe	Arg
				365					370					375
Pro	Thr	Phe	Pro	Ala	Ser	Ser	Pro	Tyr	Val	Thr	Thr	Val	Gly	Gly
				380					385					390
Thr	Ser	Phe	Gln	Glu	Pro	Phe	Leu	Ile	Thr	Asn	Glu	Ile	Val	Asp
				395					400					405
Tyr	Ile	Ser	Gly	Gly	Gly	Phe	Ser	Asn	Val	Phe	Pro	Arg	Pro	Ser
				410					415					420
Tyr	Gln	Glu	Glu	Ala	Val	Thr	Lys	Phe	Leu	Ser	Ser	Ser	Pro	His
				425					430					435
Leu	Pro	Pro	Ser	Ser	Tyr	Phe	Asn	Ala	Ser	Gly	Arg	Ala	Tyr	Pro
				440					445					450
Asp	Val	Ala	Ala	Leu	Ser	Asp	Gly	Tyr	Trp	Val	Val	Ser	Asn	Arg
				455					460					465
Val	Pro	Ile	Pro	Trp	Val	Ser	Gly	Thr	Ser	Ala	Ser	Thr	Pro	Val
				470					475					480
Phe	Gly	Gly	Ile	Leu	Ser	Leu	Ile	Asn	Glu	His	Arg	Ile	Leu	Ser
				485					490					495
Gly	Arg	Pro	Pro	Leu	Gly	Phe	Leu	Asn	Pro	Arg	Leu	Tyr	Gln	Gln
				500					505					510
His	Gly	Ala	Gly	Leu	Phe	Asp	Val	Thr	Arg	Gly	Cys	His	Glu	Ser
				515					520					525
Cys	Leu	Asp	Glu	Glu	Val	Glu	Gly	Gln	Gly	Phe	Cys	Ser	Gly	Pro
				530					535					540
Gly	Trp	Asp	Pro	Val	Thr	Gly	Trp	Gly	Thr	Pro	Thr	Ser	Gln	Leu
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<210> 260
<211> 1638
<212> DNA
<213> Homo Sapien
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<400> 260  
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attccagggc tctcttctct tctcttcttt ctgctctgtg ctgttgggca 150  
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tccctgtcgt cttgccccag tctaccctca atttagccaa gccagacttt 250  
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gtgaagtatt ccacgggctg caccggcacc ctggtggcag agaagcatgt 600  
cctcacagct gcccaactgca tacacgatgg aaaaacctat gtgaaaggaa 650  
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cgagggggcca acgactccac ttcagccatg cccgagcaga tgaaatttca 750  
gtggatccgg gtgaaacgca cccatgtgcc caagggttg atcaagggca 800  
atgccaatga catcggcatg gattatgatt atgccctcct ggaactcaaa 850  
aagccccaca agagaaaatt tatgaagatt ggggtgagcc ctcttgctaa 900  
gcagctgcca gggggcagaa ttcacttctc tggttatgac aatgaccgac 950  
caggcaattt ggtgtatcgc ttctgtgacg tcaaagacga gacctatgac 1000  
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 ccaaattggt ttttgtcatt ggcgtgcaca cgtgtgtgtg tgtgtgtgtg 1350  
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 tgactggctt tactatttga aaactgggtt gtgtatcata tcatatatca 1450  
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 tttggggcaa tgaggaatat ttgacaatta agttaatctt cacgtttttg 1550  
 caaactttga tttttatttc atctgaactt gtttcaaaga tttatattaa 1600  
 atatttggca tacaagagat atgaaaaaaaa aaaaaaaaa 1638

<210> 261

<211> 383

<212> PRT

<213> Homo Sapien

<400> 261

Met	Ala	Gly	Ile	Pro	Gly	Leu	Leu	Phe	Leu	Leu	Phe	Phe	Leu	Leu	1	5	10	15
Cys	Ala	Val	Gly	Gln	Val	Ser	Pro	Tyr	Ser	Ala	Pro	Trp	Lys	Pro	20	25	30	
Thr	Trp	Pro	Ala	Tyr	Arg	Leu	Pro	Val	Val	Leu	Pro	Gln	Ser	Thr	35	40	45	
Leu	Asn	Leu	Ala	Lys	Pro	Asp	Phe	Gly	Ala	Glu	Ala	Lys	Leu	Glu	50	55	60	
Val	Ser	Ser	Ser	Cys	Gly	Pro	Gln	Cys	His	Lys	Gly	Thr	Pro	Leu	65	70	75	
Pro	Thr	Tyr	Glu	Glu	Ala	Lys	Gln	Tyr	Leu	Ser	Tyr	Glu	Thr	Leu	80	85	90	
Tyr	Ala	Asn	Gly	Ser	Arg	Thr	Glu	Thr	Gln	Val	Gly	Ile	Tyr	Ile	95	100	105	
Leu	Ser	Ser	Ser	Gly	Asp	Gly	Ala	Gln	His	Arg	Asp	Ser	Gly	Ser	110	115	120	

000004.071301



Ser	Gly	Lys	Ser	Arg 125	Arg	Lys	Arg	Gln	Ile 130	Tyr	Gly	Tyr	Asp	Ser 135
Arg	Phe	Ser	Ile	Phe 140	Gly	Lys	Asp	Phe	Leu 145	Leu	Asn	Tyr	Pro	Phe 150
Ser	Thr	Ser	Val	Lys 155	Leu	Ser	Thr	Gly	Cys 160	Thr	Gly	Thr	Leu	Val 165
Ala	Glu	Lys	His	Val 170	Leu	Thr	Ala	Ala	His 175	Cys	Ile	His	Asp	Gly 180
Lys	Thr	Tyr	Val	Lys 185	Gly	Thr	Gln	Lys	Leu 190	Arg	Val	Gly	Phe	Leu 195
Lys	Pro	Lys	Phe	Lys 200	Asp	Gly	Gly	Arg	Gly 205	Ala	Asn	Asp	Ser	Thr 210
Ser	Ala	Met	Pro	Glu 215	Gln	Met	Lys	Phe	Gln 220	Trp	Ile	Arg	Val	Lys 225
Arg	Thr	His	Val	Pro 230	Lys	Gly	Trp	Ile	Lys 235	Gly	Asn	Ala	Asn	Asp 240
Ile	Gly	Met	Asp	Tyr 245	Asp	Tyr	Ala	Leu	Leu 250	Glu	Leu	Lys	Lys	Pro 255
His	Lys	Arg	Lys	Phe 260	Met	Lys	Ile	Gly	Val 265	Ser	Pro	Pro	Ala	Lys 270
Gln	Leu	Pro	Gly	Gly 275	Arg	Ile	His	Phe	Ser 280	Gly	Tyr	Asp	Asn	Asp 285
Arg	Pro	Gly	Asn	Leu 290	Val	Tyr	Arg	Phe	Cys 295	Asp	Val	Lys	Asp	Glu 300
Thr	Tyr	Asp	Leu	Leu 305	Tyr	Gln	Gln	Cys	Asp 310	Ala	Gln	Pro	Gly	Ala 315
Ser	Gly	Ser	Gly	Val 320	Tyr	Val	Arg	Met	Trp 325	Lys	Arg	Gln	Gln	Gln 330
Lys	Trp	Glu	Arg	Lys 335	Ile	Ile	Gly	Ile	Phe 340	Ser	Gly	His	Gln	Trp 345
Val	Asp	Met	Asn	Gly 350	Ser	Pro	Gln	Asp	Phe 355	Asn	Val	Ala	Val	Arg 360
Ile	Thr	Pro	Leu	Lys 365	Tyr	Ala	Gln	Ile	Cys 370	Tyr	Trp	Ile	Lys	Gly 375
Asn	Tyr	Leu	Asp	Cys 380	Arg	Glu	Gly							



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caggatacct gttccccag cctgtgggaa gccccagcag ctgaaccggg 200
ttgtgggchg cgaggacagc actgacagcg agtggccctg gatcgtgagc 250
atccagaaga atgggacca ccactgcgca ggttctctgc tcaccagccg 300
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cgggtcccaga aggtgggtgt tgccctgggtg gagccccacc ctgtgtattc 450
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ggacagggac ccatactga ggacatgctg tgtgccggct acttgagggg 750
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<210> 263
<211> 317
<212> PRT
<213> Homo Sapien.
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Met	Val	Val	Ser	Gly	Ala	Pro	Pro	Ala	Leu	Gly	Gly	Gly	Cys	Leu
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Gly	Thr	Phe	Thr	Ser	Leu	Leu	Leu	Leu	Ala	Ser	Thr	Ala	Ile	Leu
				20					25					30
Asn	Ala	Ala	Arg	Ile	Pro	Val	Pro	Pro	Ala	Cys	Gly	Lys	Pro	Gln
				35					40					45
Gln	Leu	Asn	Arg	Val	Val	Gly	Gly	Glu	Asp	Ser	Thr	Asp	Ser	Glu
				50					55					60
Trp	Pro	Trp	Ile	Val	Ser	Ile	Gln	Lys	Asn	Gly	Thr	His	His	Cys
				65					70					75
Ala	Gly	Ser	Leu	Leu	Thr	Ser	Arg	Trp	Val	Ile	Thr	Ala	Ala	His
				80					85					90
Cys	Phe	Lys	Asp	Asn	Leu	Asn	Lys	Pro	Tyr	Leu	Phe	Ser	Val	Leu
				95					100					105
Leu	Gly	Ala	Trp	Gln	Leu	Gly	Asn	Pro	Gly	Ser	Arg	Ser	Gln	Lys
				110					115					120
Val	Gly	Val	Ala	Trp	Val	Glu	Pro	His	Pro	Val	Tyr	Ser	Trp	Lys
				125					130					135
Glu	Gly	Ala	Cys	Ala	Asp	Ile	Ala	Leu	Val	Arg	Leu	Glu	Arg	Ser
				140					145					150
Ile	Gln	Phe	Ser	Glu	Arg	Val	Leu	Pro	Ile	Cys	Leu	Pro	Asp	Ala
				155					160					165
Ser	Ile	His	Leu	Pro	Pro	Asn	Thr	His	Cys	Trp	Ile	Ser	Gly	Trp
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Arg Ser

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<213> Artificial Sequence

<223> Synthetic Oligonucleotide Probe

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<213> Art

<223> Synthetic Oligonucleotide Probe

gcagaggtgt ctaagggttg 19

<211> 24



<213> Artificial Sequence

<223> Synthetic Oligonucleotide Probe

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<211> 45

<213> Artificial Sequence

<223> Synthetic Oligonucleotide Probe

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<211> 24

<213> Artificial Sequence

<223> Synthetic Oligonucleotide Probe

gaatgccctg caagcatcaa ctgg 24

<211> 50

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<223> Synthetic Oligonucleotide Probe

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<210> 277  
<211> 18  
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<210> 279  
<211> 24  
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<400> 279  
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<213> Artificial Sequence

<220>

103740-102666



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<210> 285
<211> 463
<212> PRT
<213> Homo Sapien
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Glu Glu Lys Arg Leu Met Val Glu Leu His Asn Leu Tyr Arg Ala
      35                      40              45

Gln Val Ser Pro Thr Ala Ser Asp Met Leu His Met Arg Trp Asp
      50                      55              60

Glu Glu Leu Ala Ala Phe Ala Lys Ala Tyr Ala Arg Gln Cys Val
      65                      70              75

Trp Gly His Asn Lys Glu Arg Gly Arg Arg Gly Glu Asn Leu Phe
      80                      85              90

Ala Ile Thr Asp Glu Gly Met Asp Val Pro Leu Ala Met Glu Glu
      95                     100             105

Trp His His Glu Arg Glu His Tyr Asn Leu Ser Ala Ala Thr Cys
     110                     115             120

Ser Pro Gly Gln Met Cys Gly His Tyr Thr Gln Val Val Trp Ala
     125                     130             135
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Lys	Thr	Glu	Arg	Ile	Gly	Cys	Gly	Ser	His	Phe	Cys	Glu	Lys	Leu
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Gln	Gly	Val	Glu	Glu	Thr	Asn	Ile	Glu	Leu	Leu	Val	Cys	Asn	Tyr
				155					160					165
Glu	Pro	Pro	Gly	Asn	Val	Lys	Gly	Lys	Arg	Pro	Tyr	Gln	Glu	Gly
				170					175					180
Thr	Pro	Cys	Ser	Gln	Cys	Pro	Ser	Gly	Tyr	His	Cys	Lys	Asn	Ser
				185					190					195
Leu	Cys	Glu	Pro	Ile	Gly	Ser	Pro	Glu	Asp	Ala	Gln	Asp	Leu	Pro
				200					205					210
Tyr	Leu	Val	Thr	Glu	Ala	Pro	Ser	Phe	Arg	Ala	Thr	Glu	Ala	Ser
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Asp	Ser	Arg	Lys	Met	Gly	Thr	Pro	Ser	Ser	Leu	Ala	Thr	Gly	Ile
				230					235					240
Pro	Ala	Phe	Leu	Val	Thr	Glu	Val	Ser	Gly	Ser	Leu	Ala	Thr	Lys
				245					250					255
Ala	Leu	Pro	Ala	Val	Glu	Thr	Gln	Ala	Pro	Thr	Ser	Leu	Ala	Thr
				260					265					270
Lys	Asp	Pro	Pro	Ser	Met	Ala	Thr	Glu	Ala	Pro	Pro	Cys	Val	Thr
				275					280					285
Thr	Glu	Val	Pro	Ser	Ile	Leu	Ala	Ala	His	Ser	Leu	Pro	Ser	Leu
				290					295					300
Asp	Glu	Glu	Pro	Val	Thr	Phe	Pro	Lys	Ser	Thr	His	Val	Pro	Ile
				305					310					315
Pro	Lys	Ser	Ala	Asp	Lys	Val	Thr	Asp	Lys	Thr	Lys	Val	Pro	Ser
				320					325					330
Arg	Ser	Pro	Glu	Asn	Ser	Leu	Asp	Pro	Lys	Met	Ser	Leu	Thr	Gly
				335					340					345
Ala	Arg	Glu	Leu	Leu	Pro	His	Ala	Gln	Glu	Glu	Ala	Glu	Ala	Glu
				350					355					360
Ala	Glu	Leu	Pro	Pro	Ser	Ser	Glu	Val	Leu	Ala	Ser	Val	Phe	Pro
				365					370					375
Ala	Gln	Asp	Lys	Pro	Gly	Glu	Leu	Gln	Ala	Thr	Leu	Asp	His	Thr
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Gly	His	Thr	Ser	Ser	Lys	Ser	Leu	Pro	Asn	Phe	Pro	Asn	Thr	Ser
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gcatttaa atcatcaagcc ttttgtgcga ttgccagcta aaatggctcc 1250  
cacagtgggt ggcgga aaac aactttcaga gctttgtaaa tgccagttgt 1300  
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[illegible]



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<211> 1059
<212> PRT
<213> Homo Sapien
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Ile Ser Arg Pro Asp Leu Ser His Asn Arg Leu Ser Phe Ile Lys
                20                25                30

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Ala	Ser	Ser	Met	Ser	His	Leu	Gln	Ser	Leu	Arg	Glu	Val	Lys	Leu	
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Asn	Asn	Asn	Glu	Leu	Glu	Thr	Ile	Pro	Asn	Leu	Gly	Pro	Val	Ser	
				50					55					60	
Ala	Asn	Ile	Thr	Leu	Leu	Ser	Leu	Ala	Gly	Asn	Arg	Ile	Val	Glu	
				65					70					75	
Ile	Leu	Pro	Glu	His	Leu	Lys	Glu	Phe	Gln	Ser	Leu	Glu	Thr	Leu	
				80					85					90	
Asp	Leu	Ser	Ser	Asn	Asn	Ile	Ser	Glu	Leu	Gln	Thr	Ala	Phe	Pro	
				95					100					105	
Ala	Leu	Gln	Leu	Lys	Tyr	Leu	Tyr	Leu	Asn	Ser	Asn	Arg	Val	Thr	
				110					115					120	
Ser	Met	Glu	Pro	Gly	Tyr	Phe	Asp	Asn	Leu	Ala	Asn	Thr	Leu	Leu	
				125					130					135	
Val	Leu	Lys	Leu	Asn	Arg	Asn	Arg	Ile	Ser	Ala	Ile	Pro	Pro	Lys	
				140					145					150	
Met	Phe	Lys	Leu	Pro	Gln	Leu	Gln	His	Leu	Glu	Leu	Asn	Arg	Asn	
				155					160					165	
Lys	Ile	Lys	Asn	Val	Asp	Gly	Leu	Thr	Phe	Gln	Gly	Leu	Gly	Ala	
				170					175					180	
Leu	Lys	Ser	Leu	Lys	Met	Gln	Arg	Asn	Gly	Val	Thr	Lys	Leu	Met	
				185					190					195	
Asp	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Asn	Met	Glu	Ile	Leu	Gln	Leu	
				200					205					210	
Asp	His	Asn	Asn	Leu	Thr	Glu	Ile	Thr	Lys	Gly	Trp	Leu	Tyr	Gly	
				215					220					225	
Leu	Leu	Met	Leu	Gln	Glu	Leu	His	Leu	Ser	Gln	Asn	Ala	Ile	Asn	
				230					235					240	
Arg	Ile	Ser	Pro	Asp	Ala	Trp	Glu	Phe	Cys	Gln	Lys	Leu	Ser	Glu	
				245					250					255	
Leu	Asp	Leu	Thr	Phe	Asn	His	Leu	Ser	Arg	Leu	Asp	Asp	Ser	Ser	
				260					265					270	
Phe	Leu	Gly	Leu	Ser	Leu	Leu	Asn	Thr	Leu	His	Ile	Gly	Asn	Asn	
				275					280					285	
Arg	Val	Ser	Tyr	Ile	Ala	Asp	Cys	Ala	Phe	Arg	Gly	Leu	Ser	Ser	



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Leu Lys Thr Leu Asp Leu Lys Asn Asn 305	Glu Ile Ser Trp Thr Ile 310	315
Glu Asp Met Asn Gly Ala Phe Ser Gly 320	Leu Asp Lys Leu Arg Arg 325	330
Leu Ile Leu Gln Gly Asn Arg Ile Arg 335	Ser Ile Thr Lys Lys Ala 340	345
Phe Thr Gly Leu Asp Ala Leu Glu His 350	Leu Asp Leu Ser Asp Asn 355	360
Ala Ile Met Ser Leu Gln Gly Asn Ala 365	Phe Ser Gln Met Lys Lys 370	375
Leu Gln Gln Leu His Leu Asn Thr Ser 380	Ser Leu Leu Cys Asp Cys 385	390
Gln Leu Lys Trp Leu Pro Gln Trp Val 395	Ala Glu Asn Asn Phe Gln 400	405
Ser Phe Val Asn Ala Ser Cys Ala His 410	Pro Gln Leu Leu Lys Gly 415	420
Arg Ser Ile Phe Ala Val Ser Pro Asp 425	Gly Phe Val Cys Asp Asp 430	435
Phe Pro Lys Pro Gln Ile Thr Val Gln 440	Pro Glu Thr Gln Ser Ala 445	450
Ile Lys Gly Ser Asn Leu Ser Phe Ile 455	Cys Ser Ala Ala Ser Ser 460	465
Ser Asp Ser Pro Met Thr Phe Ala Trp 470	Lys Lys Asp Asn Glu Leu 475	480
Leu His Asp Ala Glu Met Glu Asn Tyr 485	Ala His Leu Arg Ala Gln 490	495
Gly Gly Glu Val Met Glu Tyr Thr Thr 500	Ile Leu Arg Leu Arg Glu 505	510
Val Glu Phe Ala Ser Glu Gly Lys Tyr 515	Gln Cys Val Ile Ser Asn 520	525
His Phe Gly Ser Ser Tyr Ser Val Lys 530	Ala Lys Leu Thr Val Asn 535	540
Met Leu Pro Ser Phe Thr Lys Thr Pro 545	Met Asp Leu Thr Ile Arg 550	555

100T-20-1026060



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 575 580 585  
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 Cys Thr Ala Gln Asn Ser Ala Gly Ser Ile Ser Ala Asn Ala Thr  
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 Pro Leu Val Val Thr Glu Arg His Phe Phe Ala Ala Gly Asn Gln  
 680 685 690  
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 Thr Ala Pro Ser Leu Asp Asp Asp Gly Trp Ala Thr Val Gly Val  
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 Trp Val Val Ile Ile Tyr His Thr Arg Arg Arg Asn Glu Asp Cys  
 770 775 780  
 Ser Ile Thr Asn Thr Asp Glu Thr Asn Leu Pro Ala Asp Ile Pro  
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 Ser Tyr Leu Ser Ser Gln Gly Thr Leu Ala Asp Arg Gln Asp Gly  
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 830 835 840  
 Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr  
 845 850 855  
 Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr  
 860 865 870  
 Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His  
 875 880 885  
 Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr  
 890 895 900  
 Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His  
 905 910 915  
 Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp  
 920 925 930  
 Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn  
 935 940 945  
 Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu  
 950 955 960  
 Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn  
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 Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu  
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 995 1000 1005  
 Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly  
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 His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro  
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&lt;210&gt; 291

&lt;211&gt; 2906

FBI LABORATORY



&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 291

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FOOTNOTES



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Ser Arg Lys Arg Leu Ala Arg Leu Pro Glu Pro Leu Pro Ser Trp  
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Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser  
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FBI LABORATORY



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<210> 315
<211> 509
<212> PRT
<213> Homo Sapien
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Ser Ser Ile Gly Leu Cys Arg Tyr Gly Gly Arg Ile Asp Cys Cys
                35                    40                    45

Trp Gly Trp Ala Arg Gln Ser Trp Gly Gln Cys Gln Pro Val Cys
                50                    55                    60

Gln Pro Arg Cys Lys His Gly Glu Cys Ile Gly Pro Asn Lys Cys
                65                    70                    75

Lys Cys His Pro Gly Tyr Ala Gly Lys Thr Cys Asn Gln Asp Leu
                80                    85                    90

Asn Glu Cys Gly Leu Lys Pro Arg Pro Cys Lys His Arg Cys Met
                95                    100                    105

Asn Thr Tyr Gly Ser Tyr Lys Cys Tyr Cys Leu Asn Gly Tyr Met
                110                    115                    120

Leu Met Pro Asp Gly Ser Cys Ser Ser Ala Leu Thr Cys Ser Met
                125                    130                    135

Ala Asn Cys Gln Tyr Gly Cys Asp Val Val Lys Gly Gln Ile Arg
                140                    145                    150

Cys Gln Cys Pro Ser Pro Gly Leu His Leu Ala Pro Asp Gly Arg
                155                    160                    165

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Thr Cys Val Asp Val Asp Glu Cys Ala Thr Gly Arg Ala Ser Cys	170	175	180
Pro Arg Phe Arg Gln Cys Val Asn Thr Phe Gly Ser Tyr Ile Cys	185	190	195
Lys Cys His Lys Gly Phe Asp Leu Met Tyr Ile Gly Gly Lys Tyr	200	205	210
Gln Cys His Asp Ile Asp Glu Cys Ser Leu Gly Gln Tyr Gln Cys	215	220	225
Ser Ser Phe Ala Arg Cys Tyr Asn Val Arg Gly Ser Tyr Lys Cys	230	235	240
Lys Cys Lys Glu Gly Tyr Gln Gly Asp Gly Leu Thr Cys Val Tyr	245	250	255
Ile Pro Lys Val Met Ile Glu Pro Ser Gly Pro Ile His Val Pro	260	265	270
Lys Gly Asn Gly Thr Ile Leu Lys Gly Asp Thr Gly Asn Asn Asn	275	280	285
Trp Ile Pro Asp Val Gly Ser Thr Trp Trp Pro Pro Lys Thr Pro	290	295	300
Tyr Ile Pro Pro Ile Ile Thr Asn Arg Pro Thr Ser Lys Pro Thr	305	310	315
Thr Arg Pro Thr Pro Lys Pro Thr Pro Ile Pro Thr Pro Pro Pro	320	325	330
Pro Pro Pro Leu Pro Thr Glu Leu Arg Thr Pro Leu Pro Pro Thr	335	340	345
Thr Pro Glu Arg Pro Thr Thr Gly Leu Thr Thr Ile Ala Pro Ala	350	355	360
Ala Ser Thr Pro Pro Gly Gly Ile Thr Val Asp Asn Arg Val Gln	365	370	375
Thr Asp Pro Gln Lys Pro Arg Gly Asp Val Phe Ser Val Leu Val	380	385	390
His Ser Cys Asn Phe Asp His Gly Leu Cys Gly Trp Ile Arg Glu	395	400	405
Lys Asp Asn Asp Leu His Trp Glu Pro Ile Arg Asp Pro Ala Gly	410	415	420
Gly Gln Tyr Leu Thr Val Ser Ala Ala Lys Ala Pro Gly Gly Lys			



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<210> 316
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 316
gatggttcct gctcaagtgc cctg 24

<210> 317
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 317
ttgcacttgt aggacccacg tacg 24

<210> 318
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 318
ctgatggggag gacctgtgta gatgttgatg aatgtgctac aggaagagcc 50

<210> 319
<211> 2110
<212> DNA

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&lt;213&gt; Homo Sapien

&lt;400&gt; 319

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<210> 320
<211> 450
<212> PRT
<213> Homo Sapien
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                20           25         30

Gly Val Arg Gly Gln Ala Leu Tyr Leu Pro Val His Tyr Gly Phe
               35           40         45

His Thr Pro Ala Ser Asp Ile Gln Ile Ile Trp Leu Phe Glu Arg
              50           55         60
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Pro His Thr Met Pro Lys Tyr Leu Leu Gly Ser Val Asn Lys Ser  
 65 70 75  
 Val Val Pro Asp Leu Glu Tyr Gln His Lys Phe Thr Met Met Pro  
 80 85 90  
 Pro Asn Ala Ser Leu Leu Ile Asn Pro Leu Gln Phe Pro Asp Glu  
 95 100 105  
 Gly Asn Tyr Ile Val Lys Val Asn Ile Gln Gly Asn Gly Thr Leu  
 110 115 120  
 Ser Ala Ser Gln Lys Ile Gln Val Thr Val Asp Asp Pro Val Thr  
 125 130 135  
 Lys Pro Val Val Gln Ile His Pro Pro Ser Gly Ala Val Glu Tyr  
 140 145 150  
 Val Gly Asn Met Thr Leu Thr Cys His Val Glu Gly Gly Thr Arg  
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 Leu Ala Tyr Gln Trp Leu Lys Asn Gly Arg Pro Val His Thr Ser  
 170 175 180  
 Ser Thr Tyr Ser Phe Ser Pro Gln Asn Asn Thr Leu His Ile Ala  
 185 190 195  
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 200 205 210  
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 Tyr Tyr Gly Pro Tyr Gly Leu Gln Val Asn Ser Asp Lys Gly Leu  
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 Lys Val Gly Glu Val Phe Thr Val Asp Leu Gly Glu Ala Ile Leu  
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 260 265 270  
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Lys Lys Tyr Gln Pro Tyr Lys Val Ile Lys Gln Lys Leu Glu Gly		
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&lt;210&gt; 321

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 321

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&lt;210&gt; 322

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 322

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&lt;210&gt; 323

&lt;211&gt; 45

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

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<211> 2397

<213> Homo Sapien

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gacgtgccat aactacttta ttgaagacct tggattgcc a gtgtggggat 550
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tttggtgtg taacttgtga tgccttagaa aaatatccta agcacaaaat 2350



Arg Arg Arg Pro Gln Pro Tyr Pro Tyr Pro Ser Lys Lys Leu Leu



	215	220	225
Ser Glu Ser Ala Gln Pro Leu Lys Lys Val Glu Glu Glu Gln Glu			
	230	235	240
Ala Asp Glu Glu Asp Val Ser Glu Glu Glu Ala Glu Ser Lys Glu			
	245	250	255
Gly Thr Asn Lys Asp Phe Pro Gln Asn Ala Ile Arg Gln Arg Ser			
	260	265	270
Leu Gly Pro Ser Leu Ala Thr Asp Lys Ser			
	275	280	

&lt;210&gt; 326

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 326

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&lt;210&gt; 327

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 327

tatgtggatc aggacgtgcc 20

&lt;210&gt; 328

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 328

tgcagggttc agtctagatt g 21

&lt;210&gt; 329

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

P03104.1



<223> Synthetic Oligonucleotide Probe

ttgaaggaca aaggcaatct gccac 25

<211> 45

<213> Artificial Sequence

<223> Synthetic Oligonucleotide Probe

<400> 330  
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<211> 2168

<213> Homo Sapien

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acttccctct gtgaccatga aactctgggt gtctgcattg ctgatggcct 200
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gttagctgtc tagcgcttag caagggtgct ttgtacctca ggtgttttag 2050  
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<210> 332
<211> 533
<212> PRT
<213> Homo Sapien
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Thr Asp Leu Ile Tyr Ala Glu Lys Glu Leu Val Gln Ser Leu Lys
                      35                      40                      45

Glu Tyr Ile Leu Val Glu Glu Ala Lys Leu Ser Lys Ile Lys Ser
                      50                      55                      60

Trp Ala Asn Lys Met Glu Ala Leu Thr Ser Lys Ser Ala Ala Asp
                      65                      70                      75

Ala Glu Gly Tyr Leu Ala His Pro Val Asn Ala Tyr Lys Leu Val
                      80                      85                      90

Lys Arg Leu Asn Thr Asp Trp Pro Ala Leu Glu Asp Leu Val Leu
                      95                      100                      105

Gln Asp Ser Ala Ala Gly Phe Ile Ala Asn Leu Ser Val Gln Arg
                      110                      115                      120

Gln Phe Phe Pro Thr Asp Glu Asp Glu Ile Gly Ala Ala Lys Ala
                      125                      130                      135

Leu Met Arg Leu Gln Asp Thr Tyr Arg Leu Asp Pro Gly Thr Ile
                      140                      145                      150

Ser Arg Gly Glu Leu Pro Gly Thr Lys Tyr Gln Ala Met Leu Ser
                      155                      160                      165

Val Asp Asp Cys Phe Gly Met Gly Arg Ser Ala Tyr Asn Glu Gly
                      170                      175                      180

Asp Tyr Tyr His Thr Val Leu Trp Met Glu Gln Val Leu Lys Gln
                      185                      190                      195

Leu Asp Ala Gly Glu Glu Ala Thr Thr Thr Lys Ser Gln Val Leu
                      200                      205                      210

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Asp	Tyr	Leu	Ser	Tyr	Ala	Val	Phe	Gln	Leu	Gly	Asp	Leu	His	Arg	
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Ala	Leu	Glu	Leu	Thr	Arg	Arg	Leu	Leu	Ser	Leu	Asp	Pro	Ser	His	
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Glu	Arg	Ala	Gly	Gly	Asn	Leu	Arg	Tyr	Phe	Glu	Gln	Leu	Leu	Glu	
				245					250						255
Glu	Glu	Arg	Glu	Lys	Thr	Leu	Thr	Asn	Gln	Thr	Glu	Ala	Glu	Leu	
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Ala	Thr	Pro	Glu	Gly	Ile	Tyr	Glu	Arg	Pro	Val	Asp	Tyr	Leu	Pro	
				275					280						285
Glu	Arg	Asp	Val	Tyr	Glu	Ser	Leu	Cys	Arg	Gly	Glu	Gly	Val	Lys	
				290					295						300
Leu	Thr	Pro	Arg	Arg	Gln	Lys	Arg	Leu	Phe	Cys	Arg	Tyr	His	His	
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Gly	Asn	Arg	Ala	Pro	Gln	Leu	Leu	Ile	Ala	Pro	Phe	Lys	Glu	Glu	
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Asp	Glu	Trp	Asp	Ser	Pro	His	Ile	Val	Arg	Tyr	Tyr	Asp	Val	Met	
				335					340						345
Ser	Asp	Glu	Glu	Ile	Glu	Arg	Ile	Lys	Glu	Ile	Ala	Lys	Pro	Lys	
				350					355						360
Leu	Ala	Arg	Ala	Thr	Val	Arg	Asp	Pro	Lys	Thr	Gly	Val	Leu	Thr	
				365					370						375
Val	Ala	Ser	Tyr	Arg	Val	Ser	Lys	Ser	Ser	Trp	Leu	Glu	Glu	Asp	
				380					385						390
Asp	Asp	Pro	Val	Val	Ala	Arg	Val	Asn	Arg	Arg	Met	Gln	His	Ile	
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Thr	Gly	Leu	Thr	Val	Lys	Thr	Ala	Glu	Leu	Leu	Gln	Val	Ala	Asn	
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Tyr	Gly	Val	Gly	Gly	Gln	Tyr	Glu	Pro	His	Phe	Asp	Phe	Ser	Arg	
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Arg	Pro	Phe	Asp	Ser	Gly	Leu	Lys	Thr	Glu	Gly	Asn	Arg	Leu	Ala	
				440					445						450
Thr	Phe	Leu	Asn	Tyr	Met	Ser	Asp	Val	Glu	Ala	Gly	Gly	Ala	Thr	
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Val	Phe	Pro	Asp	Leu	Gly	Ala	Ala	Ile	Trp	Pro	Lys	Lys	Gly	Thr	
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<220>  
<223> Synthetic Oligonucleotide Probe



acactcagca ttgcctggta cttg 24

<211> 45

<213> Artificial Sequence

<223> Synthetic Oligonucleotide Probe

<400> 337  
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<211> 2789

<213> Homo Sapien

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agacaggaca atcttcttgg ggatgctggt cctggaagcc agcgggcctt 200
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cccgggctcc agcagggatg caggtggtgt ctcatgggga tgagcggccc 800
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<210> 339
<211> 772
<212> PRT
<213> Homo Sapien
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<400> 339
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Leu Ile Leu Gly Leu Ser Leu Gly Cys Ser Leu Ser Leu Leu Arg
                               20                               25                               30

Val Ser Trp Ile Gln Gly Glu Gly Glu Asp Pro Cys Val Glu Ala
                               35                               40                               45

Val Gly Glu Arg Gly Gly Pro Gln Asn Pro Asp Ser Arg Ala Arg
                               50                               55                               60

Leu Asp Gln Ser Asp Glu Asp Phe Lys Pro Arg Ile Val Pro Tyr
                               65                               70                               75

Tyr Arg Asp Pro Asn Lys Pro Tyr Lys Lys Val Leu Arg Thr Arg
                               80                               85                               90

Tyr Ile Gln Thr Glu Leu Gly Ser Arg Glu Arg Leu Leu Val Ala

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				95						100						105
Val	Leu	Thr	Ser	Arg	Ala	Thr	Leu	Ser	Thr	Leu	Ala	Val	Ala	Val		
				110						115				120		
Asn	Arg	Thr	Val	Ala	His	His	Phe	Pro	Arg	Leu	Leu	Tyr	Phe	Thr		
				125						130				135		
Gly	Gln	Arg	Gly	Ala	Arg	Ala	Pro	Ala	Gly	Met	Gln	Val	Val	Ser		
				140						145				150		
His	Gly	Asp	Glu	Arg	Pro	Ala	Trp	Leu	Met	Ser	Glu	Thr	Leu	Arg		
				155						160				165		
His	Leu	His	Thr	His	Phe	Gly	Ala	Asp	Tyr	Asp	Trp	Phe	Phe	Ile		
				170						175				180		
Met	Gln	Asp	Asp	Thr	Tyr	Val	Gln	Ala	Pro	Arg	Leu	Ala	Ala	Leu		
				185						190				195		
Ala	Gly	His	Leu	Ser	Ile	Asn	Gln	Asp	Leu	Tyr	Leu	Gly	Arg	Ala		
				200						205				210		
Glu	Glu	Phe	Ile	Gly	Ala	Gly	Glu	Gln	Ala	Arg	Tyr	Cys	His	Gly		
				215						220				225		
Gly	Phe	Gly	Tyr	Leu	Leu	Ser	Arg	Ser	Leu	Leu	Leu	Arg	Leu	Arg		
				230						235				240		
Pro	His	Leu	Asp	Gly	Cys	Arg	Gly	Asp	Ile	Leu	Ser	Ala	Arg	Pro		
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Asp	Glu	Trp	Leu	Gly	Arg	Cys	Leu	Ile	Asp	Ser	Leu	Gly	Val	Gly		
				260						265				270		
Cys	Val	Ser	Gln	His	Gln	Gly	Gln	Gln	Tyr	Arg	Ser	Phe	Glu	Leu		
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Ala	Lys	Asn	Arg	Asp	Pro	Glu	Lys	Glu	Gly	Ser	Ser	Ala	Phe	Leu		
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Ser	Ala	Phe	Ala	Val	His	Pro	Val	Ser	Glu	Gly	Thr	Leu	Met	Tyr		
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Arg	Leu	His	Lys	Arg	Phe	Ser	Ala	Leu	Glu	Leu	Glu	Arg	Ala	Tyr		
				320						325				330		
Ser	Glu	Ile	Glu	Gln	Leu	Gln	Ala	Gln	Ile	Arg	Asn	Leu	Thr	Val		
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Leu	Thr	Pro	Glu	Gly	Glu	Ala	Gly	Leu	Ser	Trp	Pro	Val	Gly	Leu		
				350						355				360		



Pro	Ala	Pro	Phe	Thr	Pro	His	Ser	Arg	Phe	Glu	Val	Leu	Gly	Trp	375
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Asp	Tyr	Phe	Thr	Glu	Gln	His	Thr	Phe	Ser	Cys	Ala	Asp	Gly	Ala	390
				380					385						
Pro	Lys	Cys	Pro	Leu	Gln	Gly	Ala	Ser	Arg	Ala	Asp	Val	Gly	Asp	405
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				425					430						
Phe	Asp	Pro	Ala	Arg	Gly	Met	Glu	Tyr	Thr	Leu	Asp	Leu	Leu	Leu	450
				440					445						
Glu	Cys	Val	Thr	Gln	Arg	Gly	His	Arg	Arg	Ala	Leu	Ala	Arg	Arg	465
				455					460						
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				470					475						
Pro	Tyr	Val	Thr	Glu	Ala	Thr	Arg	Val	Gln	Leu	Val	Leu	Pro	Leu	495
				485					490						
Leu	Val	Ala	Glu	Ala	Ala	Ala	Ala	Pro	Ala	Phe	Leu	Glu	Ala	Phe	510
				500					505						
Ala	Ala	Asn	Val	Leu	Glu	Pro	Arg	Glu	His	Ala	Leu	Leu	Thr	Leu	525
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Leu	Leu	Val	Tyr	Gly	Pro	Arg	Glu	Gly	Gly	Arg	Gly	Ala	Pro	Asp	540
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Pro	Phe	Leu	Gly	Val	Lys	Ala	Ala	Ala	Ala	Glu	Leu	Glu	Arg	Arg	555
				545					550						
Tyr	Pro	Gly	Thr	Arg	Leu	Ala	Trp	Leu	Ala	Val	Arg	Ala	Glu	Ala	570
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Pro	Ser	Gln	Val	Arg	Leu	Met	Asp	Val	Val	Ser	Lys	Lys	His	Pro	585
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Val	Asp	Thr	Leu	Phe	Phe	Leu	Thr	Thr	Val	Trp	Thr	Arg	Pro	Gly	600
				590					595						
Pro	Glu	Val	Leu	Asn	Arg	Cys	Arg	Met	Asn	Ala	Ile	Ser	Gly	Trp	615
				605					610						
Gln	Ala	Phe	Phe	Pro	Val	His	Phe	Gln	Glu	Phe	Asn	Pro	Ala	Leu	630
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<210> 340
<211> 1572
<212> DNA
<213> Homo Sapien
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ctttttgaag ggtgtgatgc ttggaagcat tttctgtgct ttgatcacta 150
tgctaggaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 200
catcatcacc tacaagctcc taacaaagaa gatatcttga aaatttcaga 250
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<213> Homo Sapien

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Arg	Leu	Asn	Ser	Leu	Leu	Asn	Ile	Pro	Glu	Lys	Cys	Pro	Glu	Gln	210
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<213> Homo Sapien
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Ile Leu Phe Leu Ser Ala Cys Phe Ile Thr Arg Cys Val Val Thr
          35          40          45
Phe Arg Ile Phe Gln Thr Cys Asp Glu Lys Lys Phe Gln Leu Pro
          50          55          60
Glu Asn Phe Thr Glu Leu Ser Cys Tyr Asn Tyr Gly Ser Gly Ser
          65          70          75
Val Lys Asn Cys Cys Pro Leu Asn Trp Glu Tyr Phe Gln Ser Ser
          80          85          90
Cys Tyr Phe Phe Ser Thr Asp Thr Ile Ser Trp Ala Leu Ser Leu
          95          100          105
Lys Asn Cys Ser Ala Met Gly Ala His Leu Val Val Ile Asn Ser
          110          115          120
Gln Glu Glu Gln Glu Phe Leu Ser Tyr Lys Lys Pro Lys Met Arg
          125          130          135
Glu Phe Phe Ile Gly Leu Ser Asp Gln Val Val Glu Gly Gln Trp
          140          145          150
Gln Trp Val Asp Gly Thr Pro Leu Thr Lys Ser Leu Ser Phe Trp
          155          160          165
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<220>
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<210> 389
<211> 22

<212> DNA
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<220>
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<400> 389
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<210> 390
<211> 20
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 390
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<223> Synthetic oligonucleotide probe

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<400> 419

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<400> 421  
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FOOT-20-10260660



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Gln	Val	Lys	Pro	Val	Thr	Pro	Val	Cys	Arg	Val	Pro	Lys	Ala	Val	
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His	Pro	Arg	Pro	His	Tyr	Ser	Trp	Tyr	Arg	Asn	Asp	Val	Pro	Leu	
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Pro	Thr	Asp	Ser	Arg	Ala	Asn	Pro	Arg	Phe	Arg	Asn	Ser	Ser	Phe	
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